

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2006, 18:42:00 ; Search time 5070 Seconds

(without alignments)
10090.323 Million cell updates/sec

Title: US10723681MOD.SEQ

Perfect score: 800

Sequence: 1 acattcttcaaacctctta.....caataatcagcttgatg 800

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database :

GenEmbl: *
1: gb env: *
2: gb pal: *
3: gb ph: *
4: gb pl: *
5: gb pr: *
6: gb ro: *
7: gb sta: *
8: gb sy: *
9: gb uni: *
10: gb vi: *
11: gb ov: *
12: gb hcg: *
13: gb ln: *
14: gb om: *
15: gb pa: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	798.4	99.8	120407	12 AP001967	AP001967 Homo sapi
2	798.4	99.8	165223	5 AC104059	AC104059 Homo sapi
3	796.8	99.6	175425	12 AC012208	AC012208 Homo sapi
4	397.8	49.7	401	7 G49140	G49140 SHGC-79840
5	233	29.1	206504	12 AC154950	AC154950 Bos tauru
6	113.2	14.2	181548	6 AC137121	AC137121 Mus muscu
7	110.8	13.8	206606	12 AC141145	AC141145 Rattus no
8	82.8	10.3	1422	2 BD249787	BD249787 Polydepi
9	82.8	10.3	1422	2 AR430630	AR430630 Sequence
10	82.8	10.3	1452	2 AX027295	AX027295 Sequence
11	82.8	10.3	1505	2 BD078044	BD078044 JNK3-cont
12	82.8	10.3	1505	2 CO892479	CO892479 Sequence
13	82.8	10.3	1505	2 AR380407	AR380407 Sequence
14	82.8	10.3	1505	2 AR715219	AR715219 Sequence
15	82.8	10.3	1505	2 AR377861	AR377861 Sequence
16	82.8	10.3	1505	5 HSU34819	U34819 Human JNK3
17	82.8	10.3	1850	5 BC065516	BC065516 Homo sapi
18	82.8	10.3	2095	5 AK091104	AK091104 Homo sapi

19	82.8	10.3	2211	2 CS206709	CS206709 Sequence
20	82.8	10.3	2366	2 BD078045	BD078045 JNK3-cont
21	82.8	10.3	2367	2 AR716220	AR716220 Sequence
22	82.8	10.3	2494	5 BC051731	BC051731 Homo sapi
23	82.8	10.3	2677	2 AR454561	AR454561 Sequence
24	82.8	10.3	2678	5 BC022492	BC022492 Homo sapi
25	82.8	10.3	2690	5 BC035057	BC035057 Homo sapi
26	82.8	10.3	2698	2 CS206710	CS206710 Sequence
27	82.8	10.3	3081	5 AK124791	AK124791 Homo sapi
28	80.4	10.1	1269	8 AY888567	AY888567 Synthetic
29	80.4	10.1	1269	8 AY890997	AY890997 Synthetic
30	80.4	10.1	1269	8 AY891216	AY891216 Synthetic
31	80.4	10.1	1269	8 AY893302	AY893302 Synthetic
32	80.4	10.1	1269	8 AY893752	AY893752 Synthetic
33	80.4	10.1	1269	8 BT019710	BT019710 Synthetic
34	80.4	10.1	1306	2 BD249786	BD249786 Polydepi
35	80.4	10.1	1306	2 AR430629	AR430629 Sequence
36	80.4	10.1	1306	2 AX027293	AX027293 Sequence
37	80.4	10.1	1773	2 BD078046	BD078046 JNK3-cont
38	80.4	10.1	1773	2 CO892477	CO892477 Sequence
39	80.4	10.1	1773	2 AR716221	AR716221 Sequence
40	80.4	10.1	1773	2 AX377859	AX377859 Sequence
41	80.4	10.1	2096	5 HSU34820	U34820 Human JNK3
42	80.4	10.1	2096	2 CS206708	CS206708 Sequence
43	80.4	10.1	2131	2 AR709626	AR709626 Sequence
44	80.4	10.1	2155	2 CS206711	CS206711 Sequence
45	80.4	10.1	2156	5 AK057723	AK057723 Homo sapi
46	80.4	10.1	2372	2 BD078047	BD078047 JNK3-cont
47	80.4	10.1	2372	2 BD078048	BD078048 JNK3-cont
48	80.4	10.1	2372	2 CS206708	CS206708 Sequence
49	80.4	10.1	2372	2 AR270826	AR270826 Sequence
50	80.4	10.1	2372	2 AR716222	AR716222 Sequence
51	80.4	10.1	2372	2 AR716223	AR716223 Sequence
52	80.4	10.1	2372	5 HSU07620	U07620 Human MAP k
53	80.4	10.1	2982	2 AR454560	AR454560 Sequence
54	80.4	10.1	8750	2 AX209898	AX209898 Sequence
55	68.4	8.6	1395	6 AB096077	AB096077 Mus muscu
56	68.4	8.6	1395	6 AB096079	AB096079 Mus muscu
57	68.4	8.6	2789	6 BC046625	BC046625 Mus muscu
58	66.8	8.3	1975	2 BD078049	BD078049 JNK3-cont
59	66.8	8.3	1975	2 CO892483	CO892483 Sequence
60	66.8	8.3	1975	2 AR715224	AR715224 Sequence
61	66.8	8.3	1975	2 AR377865	AR377865 Sequence
62	66.8	8.3	1975	6 RATSAPKC	RATSAPKC Rattus norv
63	66.8	8.3	1240	2 CO892481	CO892481 Sequence
64	66.8	8.2	1240	2 AX377863	AX377863 Sequence
65	66.8	8.2	1240	6 AB005665	AB005665 Mus muscu
66	66.8	8.2	1269	6 AB096076	AB096076 Mus muscu
67	66.8	8.2	1269	6 AB096078	AB096078 Mus muscu
68	64.4	8.1	2522	2 BD078050	BD078050 JNK3-cont
69	64.4	8.1	2522	2 AR716225	AR716225 Sequence
70	64.4	8.1	2522	6 MUSMAPK	MUSMAPK Mus muscu
71	58.4	7.3	1522	13 AY701231	AY701231 Orconecte
72	58.4	7.2	176250	12 CR354555	CR354555 Dario rer
73	56.4	7.0	227676	6 AC154649	AC154649 Mus muscu
74	55.8	7.0	813	7 BV654723	BV654723 S216P201
75	55.8	7.0	48787	5 DQ066599	DQ066599 Homo sapi
76	55.8	7.0	80527	5 AC092290	AC092290 Homo sapi
77	55.8	7.0	115793	5 AC104115	AC104115 Homo sapi
78	54	6.8	2918	6 BC053027	BC053027 Mus muscu
79	53.2	6.7	254280	12 AC131372	AC131372 Rattus no
80	53.2	6.7	259608	12 AC131381	AC131381 Rattus no
81	52	6.5	106753	4 AC146706	AC146706 Medicago
82	52	6.5	119559	4 AC147484	AC147484 Medicago
83	52	6.5	127651	12 AC166237	AC166237 Medicago
84	51.8	6.5	161002	12 CR759944	CR759944 Dario rer
85	51.6	6.5	1197	6 AB005663	AB005663 Mus muscu
86	50.8	6.3	1408	6 RATSAPKD	RATSAPKD Rattus norv
87	50.8	6.3	110000	12 PFMAL115	PFMAL115 Continuation (16 o
88	50.6	6.3	177324	12 BX957228	BX957228 Dario rer
89	49.6	6.2	1877	11 BC109420	BC109420 Dario rer
90	49.6	6.2	11882	13 AC115612	AC115612 Dictyoste
91	49.4	6.2	580	2 AX526055	AX526055 Sequence

92	49.4	6.2	61052	12	AC123513	Dicystose
C 93	49.4	6.2	136540	13	AC117070	Dicystose
C 94	49.2	6.2	37983	5	DD027001	Homo sapi
95	48.2	5.2	98146	5	AP002907	Homo sapi
96	48.2	5.2	146570	13	AC117076	AP117076 Dicystose
97	49.2	6.2	162130	12	AC021004	Homo sapi
C 98	49.2	6.2	220215	5	AC005708	Homo sapi
C 99	48.8	6.1	AR171430	2	AR171430	Sequence
C 100	48.8	6.1	2372	2	AX748405	Sequence

ALIGNMENTS

[illegible]

COMMENT

Gaps between the contigs are represented as 100 N.

* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

*	1	87654:	contig of 87654 bp	in length
*	87655	87754:	gap of 100 bp	
*	87755	107685:	contig of 19331 bp	in length
*	107686	107785:	gap of 100 bp	
*	107786	120407:	contig of 12622 bp	in length.

```

FEATURES
source
Location/Qualifiers
1.:120407
/organism="Homo sapiens"
/mol_type="Genomic DNA"
/db_xref="caxon:9606"
/chromosome="4"
/map="4q22-q24"
/clone="2242B18"

```

ORIGIN

Query Match	99.8%	Score 798.4	DB 12	Length 120407
Best Local Similarity	99.9%	Pred. NO. 1.5e-235		
Matches 799	Conservative	0	Mismatches 1	Indels 0
				Gaps 0

QY	1	ACATTTCTAAACCTTTATAGTGAAGCATTAGGCTTAGGAAATAATATTAGCAAT	60
Db	69526	ACATTTCTAAACCTTTATAGTGAAGCATTAGGCTTAGGAAATAATATTAGCAAT	69466

QY 61 AATAAGTAAATTGCTCAAGTCATCTAAAGCACCTTACGAGACAGTAAAAATATAT 120
Db 69466 AATAAGTAAATTGCTCAAGTCATCTAAAGCACCTTACGAGACAGTAAAAATATAT 694d

121 ATGCACAAATGCTATTAGATTCTGTGGCTAGCAACGAAAAATTTCCAAAGCTGACCTT 180

Db 69406 ATGCACATTGTGTATTAGATTCTGTGGCTAGCAACGAATAATTTCCAGCTGACCTT 69347

181 AACCGAGCCCATCTGTGATAGTTCACACTATTGTGCACATCAACCTTGAGAGATTTC 240

Db 69346 AACGGAGCCCATCTTGTHAGTGTTCACACTATTGTCACATCAACCTTGAGAGATTTC 6928

69286 AAGACCTAAGATGATGAGGAGAGGTACCGCGCTGAAGATTACTGAGCTCCACATT 69227

301 GACTTGATGTCAAAAAGGCGATTANGGCTCGAATTTTGATAGGCACATTACCTTTA 360

Db 69226 GACTTGATGCTCAAAGGCGATTATGGCTCGAATTTGATGAGCGACATTTACCCCTTAA 69167

69166 GCCCATGTTACACATTTCTTTCAGGATTCATTACTATAAAATATATATATGAAAAATTTT 69107

421 TGGCTCGATTCATTACCATCAGAAATATCAGAATGATGCCACACTGAAATATCAAAAGAA 480

Db 69106 TGTACTGATCATTTACCATCAGAAATATCAGAAATGAAATGCCACACTGAAATATCAAAAGAA 69047

481 ATAAACCTAAATCATTTATAGGACACACCATGTGATATTTGTCCATCTGCTCTTAAG 68988

541 CAATGTATGTATTCTTGCACCCCTACACAAAGGCCAAGAAATTACACAAAGTACTAG 600

Db 68986 CAATGTTATGTTATTCTTGCAACCCCTACACAAAGGCCAAGAAATTACACAAAGTACTAG. 68927

68926 TTTTGTGGCTATTCTACCGAGTGTACTCGAAGGAGGAGGCTGTCTTTTACTACACC 68867

661 ATTTTAGCTTTTCCTGSAATCACTTCCCTGTAGATAAGTCTGTAAACAAG 720

Db 68866 ATTTTAGCTTTCTTCGATTCACTACTCTCTAGATAAGTTCTGTGAAGAACAG 68807

6880c CTCGCTCTTATTAAGAAAAACAATTTATCCTTCATCCACAGGGAAATTCATTACTATATGC 68742

781 CAATATTTACGTTTGATG 800

Db 68746 CAAATATTTACGTTTGATG 68727

RESULT 2

LOCUS	AC104059	165223 bp	DNA	linear	PRI 21-FEB-2002
DEFINITION	Homo sapiens BAC clone RP13-514E23 from 4, complete sequence.				

ACCESSION	AC104059
VERSION	AC104059.5
KEYWORDS	GI:18677542
HTG	

SOURCE ORGANISM	Source Organism	Source Organism
Homo sapiens (human)	Homo sapiens (human)	Homo sapiens (human)
Homo sapiens	Homo sapiens	Homo sapiens

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Hominidae; Homo.

REFERENCE
1 (bases 1 to 105243)
AUTHORS
Sulston, J. E. and Waterston, R.
TITLE
Toward a complete human genome sequence

JOURNAL
PUBMED
Genome Res. 8 (11), 1097-1108 (1998)
9847074

AUTHORS Wang, C. and Cotton, M.
TITLE The sequence of Homo sapiens BAC clone RP13-514E23

REFERENCE
JOURNAL
Unpublished (2001)
3 (bases 1 to 165223)
WATERSON D H

TITLE Direct Submission
JOURNAL Submitted (03-DEC-2001) Genome Sequencing Center, Washington

REFERENCE
AUTHORS
TITLE
JOURNAL
4 (bases 1 to 165223)
Waterston,R.H.
Direct Submission
Submitted (15-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 165223)
Waterston,R.
Direct Submission
Submitted (12-FEB-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Feb 15, 2002 this sequence version replaced gi:18370036.

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION: Mapping information for this clone was provided by Dr. John D. McClellan, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION: The RPC1-13 Human Female BAC library was constructed using improved cloning techniques developed by Kazutoyo Osoegawa. The library was generated by Boohui Zhao in our laboratory. Construction was funded by a grant from the National Human Genome Research Institute (NHGRI, NIH) (#1R01RG01155-03). The library was generated according to the new NHGRI/DOE 'Guidance on Human Subjects in Large-scale DNA Sequencing'.

Female blood was obtained via a double-blind selection protocol. Female blood DNA was isolated from one randomly chosen donor (out of 10 female donors) and partially digested with a combination of EcoRI and EcoRI Methylase for library segments 1a2 or either MboI or PvuII for library segments 3a4. Size selected DNA was cloned into the pBAC3.6 vector between the EcoRI sites for library segments 1a2 or the BamHI sites for library segments 3a4. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). The library has been arrayed into 384-well microtiter dishes and also gridded onto 22x22cm nylon high density filters for screening by probe hybridization.

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-375K17. Actual start of this clone is at base position 1 of RP13-514E23; actual end is a base position 165223 of RP13-514E23.

Data from AC012208 was used to finish AC104059. Polymorphisms exist between AC012208 and AC104059.

FEATURES
SOURCE

```
/organism="Homo sapiens"  
/mol_type="genomic DNA"  
/db_xref="taxon:9606"
```

```

/misc_feature /chromosome="4"
repeat_region /map="4"
misc_feature /clone="RP13-514E23"
repeat_region /clone_id="RPCT-13"
repeat_region 54. .230
repeat_region /tpc_family="MIR"
repeat_region 155. .602
repeat_region /note="match to EST AI219433 (NID:g3801636) qh13405.x1"
repeat_region 375. .447
repeat_region /tpc_family="L2"
repeat_region 446. .568
repeat_region /tpc_family="L2"
repeat_region 1528. .1686
repeat_region /tpc_family=" (TAGA) n"
repeat_region 1774. .1819
repeat_region /tpc_family=" (TAGG) n"
repeat_region 1916. .2228
repeat_region /tpc_family="Alu"
repeat_region 2314. .2725
repeat_region /tpc_family="L1"
repeat_region 2741. .3010
repeat_region /tpc_family="L1"
misc_feature 2759. .3201
repeat_region /note="match to EST BI020464 (NID:g14427094)"
repeat_region 3203. .3345
misc_feature /tpc_family="L1"
misc_feature 4353. .4368
misc_feature /note="match to EST AI689229 (NID:g4900523) tx82c06.x1"
misc_feature 4353. .4368
misc_feature /note="match to EST BI963954 (NID:gl6338359) iec6b02.y1"
misc_feature 4353. .4368
misc_feature /note="match to Homo sapiens EST H19314 (NID:g885554)
misc_feature /note="similar to Homo sapiens EST B1697031
misc_feature 4602. .5135
misc_feature /note="match to EST AW264096 (NID:g6640912) qx83f12.x1"
misc_feature 4749. .5495
misc_feature /note="match to EST AI761743 (NID:g5177499) wg67g07.x1"
misc_feature 4749. .5416
misc_feature /note="similar to Mus musculus EST B1697031
misc_feature 4749. .5269
misc_feature /note="match to EST AA93990 (NID:g3180535) ou42a04.s1"
misc_feature 4749. .5200
misc_feature /note="similar to Homo sapiens EST B1520965
misc_feature (NID:g15345757)"
misc_feature 4749. .5171
misc_feature /note="similar to Mus musculus EST AA879964 (NID:g3988947)
misc_feature vwo2e03.x1"
misc_feature 4751. .5458
misc_feature /note="match to EST BG181781 (NID:g13703468) "
misc_feature 4751. .4876
misc_feature /note="match to EST BG186510 (NID:g13708197) "
misc_feature 4778. .4859
misc_feature /note="match to EST BG204046 (NID:g13725733) "
misc_feature 4794. .5096
misc_feature /note="match to EST AA216144 (NID:g1816083) "
misc_feature 4876. .5060
misc_feature /note="match to EST BG204046 (NID:g13725733) "
misc_feature 4890. .5494
misc_feature /note="similar to Mus musculus EST BM120254
misc_feature (NID:g17088280) "
misc_feature 4953. .5470
misc_feature /note="similar to Mus musculus EST AA839645 (NID:g2915740)
misc_feature vwo9g06.x1"
misc_feature 4955. .5493
misc_feature /note="match to EST AW341386 (NID:g6838012) xz99e11.x1"
misc_feature 4985. .5263
misc_feature /note="match to EST AI350609 (NID:g4087815) qg37e09.x1"
misc_feature 5041. .5493
misc_feature /note="match to EST BG576372 (NID:g13580425) "
misc_feature 5079. .5290
misc_feature /note="match to EST BG204046 (NID:g13725733) "
misc_feature 5163. .5493

```

```

misc_feature      /note="match to EST A1767905 (NID:g5234414) w199a11.x1"
5292..5586
/note="similar to Mus musculus EST BB321301
(NID:99029615)"
misc_feature      5368..5869
/note="match to EST AW401568 (NID:g6920254)"
5445..5472
repeat_region     /tpc_family="AT_rich"
6016..6179
/note="match to EST N28367 (NID:g1146603) yx26f08.r1"
6087..6807
misc_feature      /note="match to EST B1916286 (NID:g16180249)"
6183..6545
/note="similar to Homo sapiens EST AA132419 (NID:g1693910)
2007a10.r1"
6298
misc_feature      /note="match to EST BE737827 (NID:g10151819)"
6311..6864
/note="match to EST BE738433 (NID:g10152425)"
6314..6871
misc_feature      /note="match to EST BE737827 (NID:g10151819)"
6641..6790
repeat_region     /tpc_family="L2"
6830..6967
repeat_region     /tpc_family="MIR"
7012..7339
/misc_family="Alu"
7175..7217
misc_feature      /note="match to EST BF854904 (NID:g12242648)"
7364..7390
repeat_region

Query Match      99.8%; Score 798.4; DB 5; Length 165223;
Best Local Similarity 99.8%; Pred. No. 1.5e-235;
Matches 799; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ACATTTTCAAAAACCTTTATAGTAGAGCATGTCTTAGAGAAAAATATATATACATT 60
32840 ACATTTTCAAAAACCTTTATAGTAGAGCATGTCTTAGAGAAAAATATATATACATT 32899
61 AATAAGTAATTTGTCTCAAGTCATCTAAGCAATTAAGCATTAAGGATCAGTAAAAATATAT 120
32900 AATAAGTAATTTGTCTCAAGTCATCTAAGCAATTAAGGATCAGTAAAAATATATAT 32959
121 ATGCAAAATTTGTCTATTAATTTCTGTGCTAGCAAAAGAAAAATTTTCCAACTGACCTT 180
32960 ATGCAAAATTTGTCTATTAATTTCTGTGCTAGCAAAAGAAAAATTTTCCAACTGACCTT 33019
181 AACCGAGGCCATCTCTGTAGATGTTTCAACTATTGTCACTCAACCTTGAGAGAGTTC 240
33020 AACCGAGGCCATCTCTGTAGATGTTTCAACTATTGTCACTCAACCTTGAGAGAGTTC 33079
241 AAACACTAAGATGAATGAGGAGAGAGTACGGGCTGAAAGATTAAGTCTCCACATT 300
33080 AAACACTAAGATGAATGAGGAGAGAGTACGGGCTGAAAGATTAAGTCTCCACATT 33139
301 GACTTGAATGCTAAAGGCGCATTAATGCTCTGAATTTTATAGGACACTTTACCTTTA 360
33140 GACTTGAATGCTAAAGGCGCATTAATGCTCTGAATTTTATAGGACACTTTACCTTTA 33199
361 GCCCATGTTAATTTTCTTCAAGATTCATTACTATTAATTAATTTATGAAAAAGTTT 420
33200 GCCCATGTTAATTTTCTTCAAGATTCATTACTATTAATTAATTTATGAAAAAGTTT 33259
421 TGTCTGTGATCATTAACCATGAGATTAATGAGATGATGATGATGATGATGATGATGATGAT 480
33260 TGTCTGTGATCATTAACCATGAGATTAATGAGATGATGATGATGATGATGATGATGATGAT 33319
481 AAAAAAATAAATCAATTAATGAGACCAACATGATGATGATGATGATGATGATGATGATGATGAT 540
33320 AAAAAAATAAATCAATTAATGAGACCAACATGATGATGATGATGATGATGATGATGATGATGAT 33379
541 CAATGTTATGTTATTTCTTGCAACCCCTTCAACAAAGGCCAAGAAATTAACAAGTACTAG 600

```

```

Db      33380 CAATGTTATGTTATTTCTTGCAACCCCTACACAAAGGCCAAGAAATTAACAAGTACTAG 33439
Qy      601 TTTATTTGTTATTAACGAGAGAGTGAATCTGAGAGAGAGAGGCTGCTTTTACTACACC 660
Db      33440 TTTATTTGTTATTAACGAGAGAGTGAATCTGAGAGAGAGAGGCTGCTTTTACTACACC 33499
Qy      661 ATTTTATGCTTTTCTTCTGAAATTAATTAATCTCTGTTAGATTAAGTCTGTAAGAAACAG 720
Db      33500 ATTTTATGCTTTTCTTCTGAAATTAATTAATCTCTGTTAGATTAAGTCTGTAAGAAACAG 33559
Qy      721 CTGTTATTAATTAAGAAACAAATTTATCTTCATCTACACAGGAAATTAATTAATCTTAAATGC 780
Db      33560 CTGTTATTAATTAAGAAACAAATTTATCTTCATCTACACAGGAAATTAATTAATCTTAAATGC 33619
Qy      781 CAATTAATTAATGCTTTTGATG 800
Db      33620 CAATTAATTAATGCTTTTGATG 33639

RESULT 3
AC012208/c 175425 bp DNA linear HTG 26-MAY-2000
LOCUS      Homo sapiens chromosome 4 clone RP11-375K17 map 4, WORKING DRAFT
DEFINITION SEQUENCE, 12 unordered pieces.
AC012208
VERSION    AC012208.3 GI:8096853
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 175425)
Britten,B., Linton,L., Nussbaum,C., Lander,E., Allen,N., Anderson,B.,
Baldwin,J., Barne,N., Beckert,R., Bogunlavsky,L., Bokhsalter,B.,
Brown,A., Caselle,A., Colangelo,M., Collins,S., Collimore,A.,
Cooke,P., Dearrellano,K., Dewar,K., Domingo,M., Donelan,L., Doyle,M.,
Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heathford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kam,L., Karasas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., MacDonald,P., Margulis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Testaye,S., Tittel,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.U., Zimmer,A. and Zody,M.
Direct Submission
Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 26, 2000 this sequence version replaced gi:6454052.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submission@genome.wi.mit.edu
----- Project Information
Center project name: L1753
Center clone name: 375_K_17
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 144873 bases at least Q40
Consensus quality: 161974 bases at least Q30
Consensus quality: 170540 bases at least Q20

```


QY 721 CTGTGTTATATAGAAAACAATTATCTTCATCCACAGGAATTCTACTTAATGC 780
DB 136993 CTGTGTTATATAGAAAACAATTATCTTCATCCACAGGAATTCTACTTAATGC 136934
QY 781 CAATATATTACGTTTGATG 800
DB 136933 CAATATATTACGTTTGATG 136914

RESULT 4
G49140/c 401 bp DNA linear STS 30-MAR-2000
LOCUS SHGC-79940 Human Homo sapiens STS genomic, sequence tagged site.
DEFINITION G49140
ACCESSION G49140.1 GI:4529800
VERSION STS.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 401)
Olivier,M. and Cox,D.R.
Unpublished, Olivier, M., Cox, D.R. (2000)
JOURNAL Unpublished (2000)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
Tel: (650) 320-5800
Fax: (650) 320-5801
Email: Oliviereshgc.stanford.edu
Primer A: TTGTGTAGGGGTTGCCAAGAAT
Primer B: CCACATGACTGATGTCACAAA
STS size: 282

PCR Profile:
Initial incubation: 95 degrees C for 10 minutes
Denaturation: 94 degrees C for 30 seconds
Annealing: 60 degrees C for 30 seconds
Polymerization: 72 degrees C for 23 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9700

Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Amplifrag Gold Polymerase: 0.07 units/uM
Total Vol: 5 uL

Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 8.3

FEATURES
source
1..401
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="4"
/clone_11b="Human"
106..387
106..128
complement(365..387)

STS
primer_bind
primer_bind
ORIGIN

Query Match 49.7%; Score 397.8; DB 7; Length 401;
Best Local Similarity 99.5%; Pred. No. 1.9e-111;

Matches 399; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 280 AGGATTACTAGCTCCACATTGATGATGTCGAAAGGGCATTATGCTGGAATTTG 339
DB 401 AGGATTACTAGCTCCACATTGATGATGTCGAAAGGGCATTATGCTGGAATTTG 342
QY 340 ATGAGGACATTACCCTTTAGCCATGTAAACATTTCTTAGATTCATTACTATTA 399
DB 341 ATGAGGACATTACCCTTTAGCCATGTAAACATTTCTTAGATTCATTACTATTA 282
QY 400 AATTATTTATGAAAAAGTTTTGTCCTGATCATTCACATGAAATATCAGATGATG 459
DB 281 AATTATTTATGAAAAAGTTTTGTCCTGATCATTCACATGAAATATCAGATGATG 222
QY 460 CCACACTGAATATCAAAAAGAAATAACTAAATCATTTATAGACACACACCATGTGATA 519
DB 221 CCACACTGAATATCAAAAAGAAATAACTAAATCATTTATAGACACACACCATGTGATA 162
QY 520 TTGTGCCATCTGCTTTTATAGCAATGTATGTTTCTTGCAACCCCTACCAAGGCC 579
DB 161 TTGTGCCATCTGCTTTTATAGCAATGTATGTTTCTTGCAACCCCTACCAAGGCC 102
QY 580 AAGAAATTACACAAGTACTAGTTTATGTTATTCACGAGAGTACTGAGAGAGA 639
DB 101 AAGAAATTACACAAGTACTAGTTTATGTTATTCACGAGAGTACTGAGAGAGA 42
QY 640 AGGCTGCTCTTTTACTACACCATTTTATGCTTTTCTG 680
DB 41 AGGCTGCTCTTTTACTACACCATTTTATGCTTTTCTG 1

RESULT 5
AC154950 206504 bp DNA linear HTG 01-JUL-2005
LOCUS Bos taurus clone CH240-42c8, *** SEQUENCING IN PROGRESS ***
DEFINITION
AC154950
VERSION
KEYWORDS HTG, HTGS_PHASE1, HTGS_DRAFT, HTGS_ENRICHED.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 206504)
Muzny,D.Marie., Metker,M.Lee., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Albrooks,S., Amin,A., Angiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswalto,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Butrell,K., Calderon,E.,
Cadenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregorgis,E., Geer,K., Gill,R., Grady,M., Guerra,M., Guevara,W.,
Gunnarone,P., Haaland,W., Hamill,C., Hamilton,C., Hamilton,K.,
Harvey,X., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
Hollins,B., Howells,S., Huily,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpachy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levin,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuewa,L., Louisedge,H., Lozada,R.U., Lu,X., Ma,J.,
Maheshwari,M., Mahindaratne,M., Mahmood,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mahoney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,

Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
 Morgan, M., Morris, K., Morris, S., Ngunjiri, M., Murphy, M., Nair, L.,
 Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
 Nwankwelu, O., Okwuonu, G., Olarinmoye, A., Pal, S., Parks, K.,
 Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,
 Popper, F., Popdexter, A., Popovic, D., Primus, E., Pu, L.,
 Puzo, M., Quito, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,
 Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
 Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.,
 Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
 Shetty, D., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
 Sheehy, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soza, J.,
 Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
 Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umani, K.,
 Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J.,
 Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
 Williams, G., Willson, R., Wlezyk, R., Wooden, H., Worley, K.,
 Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
 Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhou, S., Dunn, D., von
 Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
 Weinstock, G. and Gibbs, R.A.
 Direct Submission
 Unpublished
 2 (bases 1 to 206504)
 Worley, K.C.
 Direct Submission
 Submitted (06-JAN-2005) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 206504)
 Cow Genome Sequencing Consortium.
 Direct Submission
 Submitted (01-JUL-2005) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jun 28, 2005 this sequence version replaced gi:57164422.
 The sequence in this assembly is a combination of BAC-based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: http://www.hgsc.bcm.tmc.edu/
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: FCBU
 Center clone name: CH240-42G8
 ----- Summary Statistics
 Assembly program: Atlas 3.0;
 Consensus quality: 195434 bases at least Q40
 Consensus quality: 197609 bases at least Q30
 Consensus quality: 199501 bases at least Q20
 Estimated insert size: 200872; sum-of-contigs estimation
 Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 29 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will

* be preserved.
 1 2091: contig of 2091 bp in length
 * 2092: gap of 871 bp
 * 2963: gap of 1741 bp in length
 * 4704: gap of 50 bp
 * 4754: contig of 1030 bp in length
 * 5784: gap of unknown length
 * 5884: contig of 673 bp in length
 * 6557: gap of 282 bp
 * 6838: gap of 11006 bp in length
 * 10956: contig of 3762 bp in length
 * 11007: gap of 50 bp
 * 14769: gap of 50 bp
 * 14818: contig of 2204 bp in length
 * 17023: gap of unknown length
 * 17123: contig of 7077 bp in length
 * 24200: gap of 50 bp
 * 24249: contig of 10444 bp in length
 * 34693: gap of 50 bp
 * 34744: gap of 6791 bp in length
 * 41534: gap of 50 bp
 * 41585: gap of 3804 bp in length
 * 45388: gap of 50 bp
 * 45438: contig of 4330 bp in length
 * 45439: gap of 50 bp
 * 49768: gap of 9640 bp in length
 * 49818: gap of 50 bp
 * 59458: gap of 50 bp
 * 59508: gap of 2348 bp in length
 * 59509: gap of 50 bp
 * 82757: gap of 20100 bp in length
 * 82807: gap of 50 bp
 * 102907: gap of 50 bp
 * 102956: gap of 50 bp
 * 102957: gap of 15597 bp in length
 * 118553: gap of 50 bp
 * 118554: gap of 2564 bp in length
 * 118604: gap of 263 bp
 * 121168: gap of 9299 bp in length
 * 121431: gap of 50 bp
 * 130730: gap of 1477 bp in length
 * 130779: gap of 50 bp
 * 145256: gap of 50 bp
 * 145257: gap of 2882 bp in length
 * 145307: gap of 50 bp
 * 173588: gap of 12049 bp in length
 * 173589: gap of 50 bp
 * 173638: gap of 50 bp
 * 173639: gap of 50 bp
 * 185687: gap of 684 bp in length
 * 185688: gap of 50 bp
 * 185737: gap of 50 bp
 * 185738: gap of 50 bp
 * 192681: gap of 50 bp
 * 192682: gap of 4585 bp in length
 * 197266: gap of 1007 bp in length
 * 197267: gap of 1007 bp in length
 * 197366: gap of 1007 bp in length
 * 198373: gap of 1007 bp in length
 * 198374: gap of 1007 bp in length
 * 198474: gap of 1564 bp in length
 * 200037: gap of 1564 bp in length
 * 200038: gap of 1564 bp in length
 * 200138: gap of 1455 bp in length
 * 201592: gap of 1455 bp in length
 * 201593: gap of 1455 bp in length
 * 201692: gap of 1455 bp in length
 * 203185: gap of 1493 bp in length
 * 203186: gap of 1493 bp in length
 * 203285: gap of 1493 bp in length
 * 203286: gap of 1493 bp in length
 * 204428: gap of 1493 bp in length
 * 204429: gap of 1493 bp in length
 * 206504: contig of 2076 bp in length.

FEATURES
 source
 1. 206504
 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /db_xref="taxon:9913"
 /clone="CH240-42G8"
 2092. 2962
 /estimated_length=871
 4704. 4753
 /estimated_length=50
 5784. 5883
 /estimated_length=unknown
 6557. 6838
 /estimated_length=282
 10957. 11006

	gap	/estimated length=50 14769 . 14818 /estimated length=50	
	gap	/estimated length=unknown 17023 . 17122	
	gap	24200 . 24249 /estimated length=50	
	gap	34694 . 34743 /estimated length=50	
	gap	41535 . 41584 /estimated length=50	
	gap	45389 . 45438 /estimated length=50	
	gap	49769 . 49818	
Query Match 29.1% Score 233; DB 12; Length 206504;			
Best Local Similarity 68.6%; Pred. No. 8,8e-61;			
Matches 477; Conservative 0; Mismatches 185; Indels 33; Gaps 10;			
Qy	115	ATATATATGCAACAATTGTGTATTAGATTCTGTGGCTAGCAACG--AAAAATTTCCAG	172
Db	11419	ATGATATGTACTAATGTGTGTCATATTGTTTGAGACTGCAAATGTAAAGATTTTCTGCG	11478
Qy	173	CTGACCTTAACCGAGGCCACTCTTGGTAGATGTTTCAACATATGTCAACATCCTTGA	232
Db	11479	CTGACTTAATATGGAACCCCGTTGGTGTAAAGGCTCAACTACTGTCACTCAACCTTAG	11538
Qy	233	AAGAGTTCAAACACTAAGAATGAATGAGGAGAGGT---ACCGGCTGAAGGATTACT	288
Db	11539	AAGAGT---AACTTATAGAGTAATGAAGGAAAAGTTTTAGGTGAGGGATTGATTCT	11595
Qy	289	GAGCTCCACATTGACTTGATGCTCAAAAGGCATATGCTCTGAATTTTGATGAGGCAC	348
Db	11596	GAACTCCACACTGAGGTGGTGGTCAAGAGGGCATTAATGATCTGAATTTTGATGAGGAC	11655
Qy	349	ATTACCCTTTAGGCCCATGTTAACATTTTCTTCAGAGTTCATTACTATTAAATTATTA	408
Db	11656	ACCAACCTTTA-----ATCAGATTAATGCTAATAATTTCTCAAGATT---CTTTGTTA	11705
Qy	409	TGAAAAGTTTGTCTCTGATCATTAACATCAAGATATACAGATGAATGCCACACTGA	468
Db	11706	TTTTAAAGTTCTGAAAAGACTCAATGCTAAATCATATTAGTCAGAAATTAATGCCACACTTA	11765
Qy	469	ATATCAAAA---GAATATAAATCTAAATCAATTATAAGGACACAAACCATGATATTGTC	525
Db	11766	CCATTCAAAAGGCGAAGAGACTGAATATCATTAAGGGAACAGGTA-ATCTAATCTGTT	11824
Qy	526	CATCTGCTTTTAAGCAATGTATGTATTTCTTTCGAACCCCTPACAAAGGCCAAGAA	585
Db	11825	CATATGCTGTGTAAGCA-----GTATATTAGTCACTCAATCTCTCTTAAGGCCAAGAAA	11879
Qy	586	TTACACAAGTACTAGTTTATTTGTTATTCACGAGAGTGAATCTCGAAGAGAAAGGCTG	645
Db	11880	ATAGGCAAGTACCGGTTGTGTGTTATTCATTGAGATGATGCTCGAAGGAAAGGCTG	11939
Qy	646	TCCTTTACTACACATTTTATAGCTTTTCTTCGAAATCATTAATCTCTGTAGATAG	705
Db	11940	TCCTTTACAAAGSCATTTCTTCGCTTTTCTTCGAGTTCAATTAATCTTATAGATAG	11939
Qy	706	TTCTGTAGAAGAACGCTGTGTTATTTATGAAAAACAATTTATCTCTTCAATCACAGGAAA	765
Db	12000	TTCTGTAAACAAA-GGTACCAAGTGTATGAAAAATCAAGTTTCTCTTAACCAAGAAAGAAA	12058
Qy	766	TTCACTACTTAATGCCAAATTAATTAAGCTTTTGATG	800
Db	12059	GTCA----TTTATTAACAAACATTAACATTTTGATG	12089
RESULT 6			
AC137121 181548 bp DNA linear ROD 16-OCT-2004			
LOCUS Mus musculus chromosome 5, clone RP23-286N22, complete sequence.			
DEFINITION AC137121			
ACCESSION			

VERSION	AC137121.9	GI:54261924
KEYWORDS	HGT.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Bukacynski, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	Blumenfeld, B., Nussbaum, C. and Lander, E.	
TITLE	Mus musculus chromosome 5, clone RP23-286M22	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 181548)	
AUTHORS	Blumenfeld, B., Nussbaum, C., Lander, E., Allen, A., Blumenfeld, S., Barnett, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Camara, J., Chang, J., Chazaro, K., Choquet, Y., Collymore, A., Cook, A., Cooke, P., DeArrelano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardys, S., Gerd, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, J., Matthews, C., McCarthy, M., Meldrum, J., Menus, L., Mihova, T., Miyauchi, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhkhong, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schaller, S., Schnuppach, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Strange-Thomann, N., Stojanovic, N., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.	
TITLE	Submitted Submission	
JOURNAL	Submitted (17-Nov-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	
REFERENCE	3 (bases 1 to 181548)	
AUTHORS	Blumenfeld, B., Nussbaum, C., Lander, E., Abouelella, A., Allen, N., Anderson, M., Anderson, S., Archibald, H.M., Barnett, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Camara, J., Chang, J., Choquet, Y., Collymore, A., Cook, A., Cooke, P., Cornum, B., DeArrelano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardys, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagos, B., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., MacDonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrum, J., Menus, L., Mihova, T., Miyauchi, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhkhong, P., Pierre, N., Rachapudi, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schaller, S., Schnuppach, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Strange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.	
TITLE	Direct Submission	
JOURNAL	Submitted (17-AUG-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	
REFERENCE	4 (bases 1 to 181548)	
AUTHORS	Blumenfeld, B., Nussbaum, C., Lander, E., Abouelella, A., Allen, N., Anderson, M., Anderson, S., Archibald, H.M., Barnett, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Camara, J., Chang, J., Choquet, Y., Collymore, A., Cook, A., Cooke, P., Cornum, B., DeArrelano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardys, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagos, B., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., MacDonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrum, J., Menus, L., Mihova, T., Miyauchi, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,	

TITLE
JOURNAL

COMMENT

Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,
 Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schnupack, R.,
 Seaman, S., Severy, P., Smith, C., Spencer, B., Strange-Thomann, N.,
 Stojanovic, N., Stubbs, M., Talamas, J., Testaye, S., Theodore, J.,
 Topham, K., Travers, M., Vasiliev, H., Venkatakrishnan, V. S., Viel, R.,
 Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L.,
 Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (16-OCT-2004) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Oct 16, 2004 this sequence version replaced gi:51315566.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/MIT Center for Genome Research
 Center code: WtBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@road.mit.edu
 ----- Project Information
 Center project name: L26408
 Center clone name: 286_M_22

FEATURES

source

----- Location/Qualifiers
 1. 181548
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /chromosome="5"
 /map="5"
 /clone="RP23-286M22"
 /clone_1lb="RPCI-23 Female Mouse BAC"
 602. 647
 /rpt_family="(TG)n"
 repeat_region
 648. 827
 /rpt_family="(TG)n"
 complement(1596..1764)
 repeat_region
 2191..2303
 /rpt_family="Tigger7"
 repeat_region
 4661..4921
 /rpt_family="(TCTCCC)n"
 repeat_region
 5655..5755
 /rpt_family="L1MB8"
 repeat_region
 5793..5863
 /rpt_family="(TG)n"
 repeat_region
 5888..6000
 /rpt_family="(TG)n"
 repeat_region
 6014..6091
 /rpt_family="(TG)n"
 repeat_region
 6153..6269
 /rpt_family="(TG)n"
 repeat_region
 6288..6311
 /rpt_family="AT_rich"
 repeat_region
 complement(6312..6758)
 /rpt_family="Lx2B"
 repeat_region
 complement(6813..6853)
 /rpt_family="B3A"
 repeat_region
 6854..6875
 /rpt_family="(TA)n"
 repeat_region
 complement(6876..7024)
 /rpt_family="B3A"
 repeat_region
 7133..7181
 /rpt_family="(GA)n"
 repeat_region
 7775..7842
 /rpt_family="(GA)n"
 repeat_region
 8626..8662
 /rpt_family="(CAA)n"
 repeat_region
 complement(11814..12121)
 /rpt_family="Lx"
 repeat_region
 12627..12694
 /rpt_family="(GCAA)n"
 repeat_region
 13907..13933

/rpt_family="(CA)n"
 14706..14843
 /rpt_family="RMR15"
 complement(15326..17003)
 repeat_region
 /rpt_family="L1VL2"
 18283..18311
 repeat_region
 /rpt_family="AT_rich"
 20110..20146
 /rpt_family="(T)n"
 20158..20182
 /rpt_family="(T)n"
 complement(20183..20327)
 repeat_region
 /rpt_family="B1_MM"
 20465..20649
 /rpt_family="L1MA6"
 20748..20905
 /rpt_family="L1MA6"
 20949..21648
 /rpt_family="L1MA6"
 21751..21847
 /rpt_family="B1_MM"
 21853..21904
 /rpt_family="(CAAAA)n"
 23773..23796
 /rpt_family="AT_rich"
 complement(24150..24474)
 repeat_region
 /rpt_family="ORR1A2"
 complement(24769..24950)
 repeat_region
 /rpt_family="B3A"
 25195..25696
 /rpt_family="RLTR11A"
 25813..25856
 /rpt_family="(CAGA)n"
 25884..25990
 /rpt_family="(GA)n"
 complement(26526..27115)
 repeat_region
 /rpt_family="L1_MM"
 27187..27472
 /rpt_family="MTE"
 complement(28452..28558)
 repeat_region
 /rpt_family="L2"
 complement(29177..29528)
 repeat_region
 /rpt_family="MT2A"
 29537..29558
 /rpt_family="AT_rich"
 29760..29936
 /rpt_family="B2_Mm2"
 29945..29982
 /rpt_family="(TAAA)n"
 30905..30939
 /rpt_family="(A)n"

Query Match 14.2%; Score 113.2; DB 6; Length 181548;
 Best Local Similarity 65.0%; Pred. No. 9,7e-24;
 Matches 238; Conservative 0; Mismatches 108; Indels 20; Gaps 4;

QY 438 ATCAAGATATATAGAAATGATATCCACATCGATATCAAAAGAAATTAATCAAT 497
 |||||
 DB 88752 ACCAAGATTTAGACGATTTGATGATGTTAAAAAATATATAAAACAAACATCGAAAT 88811
 |||||
 QY 498 ATTAAGACACACACATGATATTTGTCATCGCTCTTTAAGCAATGTTATTTTC 557
 |||||
 DB 88812 ACGGGAACCGCCATGATATCTGTTCCAGGCTCTGTGACGGCATTG-----TC 88864
 |||||
 QY 558 TTGCAACCCCTTACACAAAGGCCAAGAAATTAACAAGTACTGATTATTGTTATTCAG 617
 |||||
 DB 88865 TATGACACACACCCGTCAGAGGCGCTGA-----AGACACGAGCTTCTGTTATTCAG 88917
 |||||
 QY 618 GAGAGTGTACCTTAAGAGAGAGGCTGCTTTTACTACACATTTTATAGCTTTCTT 677
 |||||
 DB 88918 GAGAGTGTGTCTTAAGAGCGAGGCTGCTTTTACTACACATTTTATAGCTTTCTT 88977
 |||||
 QY 678 CTGAATTCATTACTCTTTGATGATAGTTCTGTA-----AGAAACAGCTGTGTATTATATA 733

```

Db      88978 CTGAGTTCATTACTCTCTGTAGTAAAGTTCTGTAATACATCAATCGCTGCTGTTATTATA 89037
QY      734 - -GAAAACAAATTATTCCTTCATCCAGCGGAATTCTACTTAAATGCCAAATTAATAC 791
Db      89038 ACAAAAGCGAAGATTCCTTAATCTACAAACCCATGAGTCGCTAAAGAAATTAATCTT 89097
QY      792 GTTTTG 797
Db      89098 TTCGTG 89103

RESULT 7.
AC141145 206606 bp DNA linear HTG 05-APR-2003
LOCUS Rattus norvegicus clone CH230-140B2, WORKING DRAFT SEQUENCE, 51
DEFINITION
unordered pieces.
AC141145
AC141145.3 GI:29568005
HTG: HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Rattus.
1 (bases 1 to 206606)
Muzny,D,Marie, Metzker,M, Lee, Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Albrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benhmed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Diya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C.M., Gabisti, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebregergis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogue, M.,
Hollins, B., Howells, S., Hu, Y., Hume, J., Idlebird, D., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karachy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorenshulte, L., Louised, H., Machado, R.J., Lu, X., Ma, J.,
Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mawliny, S., McLeod, M., McNeill, T., Meenan, S., Milosavljevic, A.,
Miner, G., Ming, E., Montemayor, J., Moore, S., Morgan, M., Morris, K.,
Morris, S., Mundasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D.,
Newton, N., Nguyen, N., Norris, S., Nwaokwelu, O., Okunodu, G.,
Olatunbosun, A., Pal, S., Parks, K., Pasternak, S., Paul, H.,
Perez, A., Perez, L., Pfankoch, C., Plopper, F., Poindexter, A.,
Popovic, D., Primus, E., Pu, L.-L., Puzo, M., Quiroz, J., Rachlin, E.,
Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A.,
Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S.,
Scott, G., Shatman, S., Shen, H., Shetty, J., Shwartsbeyn, A.,
Sison, I., Sitter, C.D., Smaj, D., Snead, A., Sodergren, E.,
Song, X.-Z., Sorelle, R., Sosa, J., Steinle, M., Strong, R., Sutton, A.,
Stvacek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S.,
Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villana, D.,
Waldron, L., Walker, B., Wang, J., Wang, O., Wang, S., Warren, J.,
Warrren, R., Wei, X., White, F., Williams, G., Willison, R., Wlezyk, R.,
Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, X.,
Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X.,
Zhao, S., Dunn, D., von Niederhansen, A., Weiss, R., Smith, D.R.,

```

```

TITLE Holt, R.A., Smith, H.O., Weinstein, G. and Gibbs, R.A.
JOURNAL Direct Submission
REFERENCE Unpublished
AUTHORS 2 (bases 1 to 206606)
Muzny, D., Mar, M., Metzker, M., Lee, A., Abramson, S., Adams, C., Alder, J.,
Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villana, D.,
Waldron, L., Walker, B., Wang, J., Wang, O., Wang, S., Warren, J.,
Warrren, R., Wei, X., White, F., Williams, G., Willison, R., Wlezyk, R.,
Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, X.,
Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X.,
Zhao, S., Dunn, D., von Niederhansen, A., Weiss, R., Smith, D.R.,
JOURNAL Submitted (10-MAR-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 206606)
Worley, K.C.
JOURNAL Direct Submission
Submitted (05-APR-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Apr 5, 2003 this sequence version replaced gi:28913113.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: KCCC
Center clone name: CH230-140B2
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 191161 bases at least Q40
Consensus quality: 195784 bases at least Q30
Consensus quality: 199697 bases at least Q20
Estimated insert size: 195646; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
-----
NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently
consists of 51 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
1
1359 1358: contig of 1358 bp in length
1459 1458: gap of unknown length
2825 2825: contig of 1367 bp in length
2925 2925: gap of unknown length
4338 4338: contig of 1413 bp in length
4438 4438: gap of unknown length
5980 5980: contig of 1542 bp in length
6080 6080: gap of unknown length
7681 7681: contig of 1601 bp in length
7781 7781: gap of unknown length
9244 9244: contig of 1463 bp in length
9344 9344: gap of unknown length
10471 10471: contig of 1127 bp in length
10571 10571: gap of unknown length
11748 11748: contig of 1177 bp in length
11848 11848: gap of unknown length
11849 11849: gap of unknown length
13253 13253: contig of 1405 bp in length
13354 13354: gap of unknown length
14587 14587: contig of 1234 bp in length
14687 14687: gap of unknown length
16037 16037: contig of 1350 bp in length
16137 16137: gap of unknown length
17435 17435: contig of 1298 bp in length
17535 17535: gap of unknown length
18972 18972: contig of 1437 bp in length
19072 19072: gap of unknown length
21193 21193: contig of 2121 bp in length
21293 21293: gap of unknown length
23612 23612: contig of 2319 bp in length

```

```
* 23613 23712: gap of unknown length
* 23713 26628: contig of 2916 bp in length
* 26629 26728: gap of unknown length
* 26729 28705: contig of 2978 bp in length
* 29707 29806: gap of unknown length
* 29807 32797: contig of 2991 bp in length
* 32798 32898: gap of unknown length
* 32899 35764: contig of 2867 bp in length
* 35765 35865: gap of unknown length
* 35866 38592: contig of 2728 bp in length
* 38593 38692: gap of unknown length
* 38693 42144: contig of 3452 bp in length
* 42145 42244: gap of unknown length
* 42245 43735: contig of 1490 bp in length
* 43736 46614: gap of unknown length
* 46615 46714: gap of unknown length
* 46715 48690: contig of 1976 bp in length
* 48691 48790: gap of unknown length
* 48791 51799: contig of 3009 bp in length
* 51800 51899: gap of unknown length
* 51900 54374: contig of 2475 bp in length
* 54375 54474: gap of unknown length
* 54475 58651: contig of 4177 bp in length
* 58652 58751: gap of unknown length
* 58752 61050: contig of 2299 bp in length
* 61051 61150: gap of unknown length
* 61151 64066: contig of 2916 bp in length
* 64067 64166: gap of unknown length
* 64167 67348: contig of 3182 bp in length
* 67349 67448: gap of unknown length
* 67449 70246: contig of 2798 bp in length
* 70247 70346: gap of unknown length
* 70347 73068: contig of 2722 bp in length
* 73069 73168: gap of unknown length
* 73169 76539: contig of 3371 bp in length
* 76540 76639: gap of unknown length
* 76640 81735: contig of 5096 bp in length
* 81736 81835: gap of unknown length
* 81836 85133: contig of 3298 bp in length
* 85134 85233: gap of unknown length
* 85234 90585: contig of 5352 bp in length
* 90586 90685: gap of unknown length
* 90686 95785: contig of 5100 bp in length
* 95786 95885: gap of unknown length
* 95886 99327: contig of 3442 bp in length
* 99328 99427: gap of unknown length
* 99428 104621: contig of 5194 bp in length
* 104622 104721: gap of unknown length
* 104722 111646: contig of 6925 bp in length
* 111647 111746: gap of unknown length
* 111747 115420: contig of 3674 bp in length
* 115421 115520: gap of unknown length
* 115521 120264: contig of 4744 bp in length
* 120265 120364: gap of unknown length
* 120365 125661: contig of 5297 bp in length
* 125662 125761: gap of unknown length
* 125762 134249: contig of 8488 bp in length
* 134250 134349: gap of unknown length
* 134350 140554: contig of 6105 bp in length
* 140555 140955: gap of unknown length
* 140956 147949: contig of 7395 bp in length
* 147950 148049: gap of unknown length
* 148050 156077: contig of 8028 bp in length
* 156078 156177: gap of unknown length
* 156178 166426: contig of 10249 bp in length
* 166427 166526: gap of unknown length
* 166527 176298: contig of 9772 bp in length
```

Query Match 13.8%; Score 110.8; DB 12; Length 206606;
Best Local Similarity 80.2%; Pred. No. 5.3e-23;
Matches 130; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

```
QY 581 AGAATTAACACAGTACTAGTTATTTGTTATTCACGGAGAGTACCTGAAGAGAA 640
DB 102768 AGGAAAGACACAGACTGCTCTTGTGTTATTCAGGAGAGTACCTGAAGGTGAG 102827
QY 641 GGCTGCTCTTTACTACACCATTTTATGCTTTTCTTGAAATTCATTACTCTGTAG 700
DB 102828 GGCTGCTCTTTACTACACCATTTTATGCTTTTCTTGAAATTCATTACTCTGTAG 102887
QY 701 ATAGTTCTGTGAAGAAACAGCTGTGTTATTTATGAAAACAA 742
DB 102888 ATAGTTCTGTGAAGAAATTAACCTCATGTGTTAGAACAGA 102929

RESULT 8
LOCUS BD249787/c 1422 bp DNA linear PAT 17-JUL-2003
DEFINITION Poly peptides derived from JNK3.
ACCESSION BD249787
VERSION BD249787.1 GI:33059557
KEYWORDS JP 2002534982-A/23.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1422)
AUTHORS Desnais,F., Fournier,A., Maury,I. and Liu,Q.Z.
TITLE Poly peptides derived from JNK3
JOURNAL Patent: JP 2002534982-A 23 22-OCT-2002;
AVENTIS PHARMA SA
COMMENT OS Homo sapiens (human)
PN JP 2002534982-A/23
PD 22-OCT-2002
PF 19-JAN-2000 JP 2000594932
PR 20-JAN-1999 FR 99/00586;26-FEB-1999 US 60/122175 P1
FRANCINE DESNAIS,ALAIN FOURNIER,ISABELLE MAURY,QING ZHOU LIU PC
C12N15/09,A61K39/395,A61K45/00,A61P7/10,A61P9/00,A61P25/00,PC
A61P25/14,
PC A61P25/16,A61P25/28,C07K16/40,C12N1/15,C12N1/19,C12N1/21 PC
C12N5/10,C12N9/12,
PC C12Q1/02,C12Q1/48,C12N15/00,C12N5/00
CC Poly peptides derived from JNK3
FH Key location/Qualifiers
FT CDS (142)..(1419).

FEATURES
source location/Qualifiers
1..1422
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="caxon:9606"

ORIGIN
Query Match 10.3%; Score 82.8; DB 2; Length 1422;
Best Local Similarity 97.7%; Pred. No. 4e-14;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTAAGTGAAGAGAGAGGCTGCTCTTTTACTATACCATTTTATGCTTTTCTTGAAATTC 685
DB 1283 GGACTGGAAGAGAGAGGCTGCTCTTTTACTATACCATTTTATGCTTTTCTTGAAATTC 1224
QY 686 ATTACTCTCTGTAGATTAAGTTCTGT 711
DB 1223 ATTACTCTCTGTAGATTAAGTTCTTT 1198

RESULT 9
LOCUS AR430630/c 1422 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 24 from patent US 6649388.
ACCESSION AR430630
VERSION AR430630.1 GI:40191471
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
```

Unclassified.
1 (bases 1 to 1422)
REFERENCE
Fournier,A., Maury,I., Zhou-Liu,Q. and Desanlis-Cremond,F.
TITLE
Polypeptides derived from JNK3
Patent: US 6649388-A 24 18-NOV-2003;
JOURNAL
Aventis Pharma S.A.; Antony;
FRX;
FEATURES
source
1. .1422
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 10.3%; Score 82.8; DB 2; Length 1422;
Best Local Similarity 97.7%; Pred. No. 4e-14;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GTACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTGCTTTCTCTGAATTC 685
1283 GCACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTGCTTTCTCTGAATTC 1224
Db 686 ATTACTCTCTGTAGATAGTCTGT 711
1223 ATTACTCTCTGTAGATAGTCTGT 1198
QY 626 GTACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTGCTTTCTCTGAATTC 685
1283 GCACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTGCTTTCTCTGAATTC 1224
Db 686 ATTACTCTCTGTAGATAGTCTGT 711
1223 ATTACTCTCTGTAGATAGTCTGT 1198
RESULT 10
AX027295/c 1422 bp DNA linear PAT 16-SEP-2000
LOCUS
Sequence 24 from Patent WO0043554.
DEFINITION
AX027295
ACCESSION
AX027295.1 GI:10188271
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1
AUTHORS
Desanlis,F., Zhou-Liu,Q., Fournier,A. and Maury,I.
TITLE
Polypeptides derived from Jnk3
Patent: WO 0043524-A 24 27-JUL-2000;
JOURNAL
AVENTIS PHARMA SA (FR) ; DESANLIS FRANCINE (FR) ; ZHOU LIU QING
(FR) ; FOURNIER ALAIN (FR) ; MAURY ISABELLE (FR)
FEATURES
source
1. .1422
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
142. .1422
/note="unamed protein product"
/codon_start=1
/protein_id="CAC09126.1"
/db_xref="GI:10188272"
/translation="MSKSKVNDQNFYSEVSDSTFTVLKRYONLKPISGAOGIVCAAY
DAVLDRNVAILKLSRPNQTHAKRAYRELIVLMCKNHKNIISLAVFPQKTLSEGO
DYLVNMLDANLCQVIOHELDHRSYLLIYOMLGGIKLHSGITIRHDLKSPNITYVK
SDCTLIKILFGIARAGTSFMTPIVATRYRAEVLILGNGYENVDIWSVGCIWSEM
VRKILFPGRDYIDWNKYIEQGTCPPEPMKLOPTVRYNRYENRKYAGLTFPKLPM
DSLFPADSEHNKAKASQARDLSKMLISYDDALQHYIINWVYDPAVEAP
POLYKOLDERETIEEMKELIYKEVNVSEKTKNGVVKQPPSGAAVNSBSLPPS
SSYNDISSNSTDQTLASDIDSLEASAGPLGCCR"
ORIGIN
Query Match 10.3%; Score 82.8; DB 2; Length 1422;
Best Local Similarity 97.7%; Pred. No. 4e-14;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GTACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTGCTTTCTCTGAATTC 685
1283 GCACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTGCTTTCTCTGAATTC 1224
Db 686 ATTACTCTCTGTAGATAGTCTGT 711
1223 ATTACTCTCTGTAGATAGTCTGT 1198

Db 1223 ATTACTCTCTGTAGATAGTCTGT 1198
RESULT 11
BD078044/c 1505 bp DNA linear PAT 27-AUG-2002
LOCUS
JNK3-controller and method of using the same.
DEFINITION
BD078044
ACCESSION
BD078044.1 GI:22623647
VERSION
JP 2001519146-A/1.
KEYWORDS
unidentified
SOURCE
unidentified
ORGANISM
unclassified sequences.
1 (bases 1 to 1505)
REFERENCE
Davis,R.J., Flavell,R.A., Rakic,P., Whitmarsh,A.J., Kuan,C.Y. and
Yang,D.D.
TITLE
JNK3-controller and method of using the same
JOURNAL
Patent: JP 2001519146-A 1 23-OCT-2001;
UNIVERSITY OF MASSACHUSETTS
COMMENT
OS Unidentified
PN JP 2001519146-A/1
PD 23-OCT-2001
PE 05-OCT-1998 JP 2000514991
PF 03-OCT-1997 US 60/060995
PI ROGER J DAVIS,RICHARD A FLAVELL,PASKO RAKIC,ALAN J WHITMARSH
PI ,CHIA YIN KUANG,
PI DERK DI YANG
PC C12N15/09,A01K67/027,A61K31/711,A61K45/00,A61K48/00,A61P9/10,
PC A61P21/00,
PC A61P25/08,A61P25/14,A61P25/16,A61P25/28,C12N5/10,C1201/48, PC
C1201/68,
PC G01N33/15,G01N33/50,C12N15/00,C12N5/00
CC Strandedness: Double;
CC Topology: Linear;
CC JNK3-controller and method of using the same
FH Key Location/Qualifiers
FT source 1. .1505
Location/Qualifiers
1. .1505
/organism="Unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 10.3%; Score 82.8; DB 2; Length 1505;
Best Local Similarity 97.7%; Pred. No. 3.9e-14;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GTACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTGCTTTCTCTGAATTC 685
1323 GCACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTGCTTTCTCTGAATTC 1264
Db 686 ATTACTCTCTGTAGATAGTCTGT 711
1263 ATTACTCTCTGTAGATAGTCTGT 1238
RESULT 12
CO892479/c 1505 bp DNA linear PAT 01-NOV-2004
LOCUS
Sequence 56 from Patent EP1469316.
DEFINITION
CO892479
ACCESSION
CO892479.1 GI:55165021
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1
AUTHORS
Weihe,E.D., Schaefer,M.K., Gillen,C., Wetzel,S. and Wendt,S.

FEATURES	University of Massachusetts and Yale University; Boston, MA
SOURCE	Location/Qualifiers 1..1505 /organism="unknown" /mol_type="genomic DNA"
ORIGIN	
Query Match	10.3%; Score 82.8; DB 2; Length 1505;
Best Local Similarity	97.7%; Pred. No. 3.9e-14;
Matches 84; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	626 GTACCTGAGAGAGAGGCTGTCTCTTTACTACACCAATTTTAAAGTCTTTCTTCGAAATTC 685
Db	1323 GCACCTGAGAGAGAGGCTGTCTCTTTACTACACCAATTTTAAAGTCTTTCTTCGAAATTC 1264
QY	686 ATTACTTCCTTTGATGATTAAGTTCTGT 711
Db	1263 ATTACTTCCTTTGATGATTAAGTTCTTT 1238
RESULT 15	
LOCUS	AX377861 1505 bp DNA linear PAT 18-MAR-2002
DEFINITION	Sequence 56 from Patent WO0212358.
ACCESSION	AX377861
VERSION	AX377861.1 GI:19573951
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
REFERENCE	1 AUTHORS : 'Gillen,C., Wetzel,E.,I., Mhendt,S., Weihe,E. and Schaefer,M.K. TITLE : Screening method JOURNAL : Patent: WO 0212358-A 56 14-FEB-2002; Gruenthal GmbH (DE) Location/Qualifiers 1..1505 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
FEATURES	
SOURCE	
ORIGIN	
Query Match	10.3%; Score 82.8; DB 2; Length 1505;
Best Local Similarity	97.7%; Pred. No. 3.9e-14;
Matches 84; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	626 GTACCTGAGAGAGAGGCTGTCTCTTTACTACACCAATTTTAAAGTCTTTCTTCGAAATTC 685
Db	1323 GCACCTGAGAGAGAGGCTGTCTCTTTACTACACCAATTTTAAAGTCTTTCTTCGAAATTC 1264
QY	686 ATTACTTCCTTTGATGATTAAGTTCTGT 711
Db	1263 ATTACTTCCTTTGATGATTAAGTTCTTT 1238
RESULT 16	
LOCUS	HSU54819/c 1505 bp mRNA linear PRI 25-JUL-1996
DEFINITION	Human JNK3 alpha2 protein kinase (JNK3A2) mRNA, complete cds.
ACCESSION	U34819
VERSION	U34819.1 GI:1463124
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 1505) Gupte,S., Barrett,T., Whitmarsh,A.J., Cavanagh,J., Sluss,H.K., Derlajd,B. and Davis,R.J. Selective interaction of JNK protein kinase isoforms with
REFERENCE	
AUTHORS	
TITLE	


```

COMMENT
OS      Unidentified
PN      JP 2001519146-A/2
PD      23-OCT-2001
PF      03-OCT-1998 JP 2000514991
PR      03-OCT-1997 US 60/060995
PI      ROGER J DAVIS, RICHARD A FLAVELL, PASKO RAKIC, ALAN J WHITMARSH
PI      CHIA YIN KUAN,
PI      DERK DI YANG
PC      C12N15/09,A01K67/027,A61K31/711,A61K45/00,A61K48/00,A61P9/10,
PC      A61P21/00,
PC      A61P25/08,A61P25/14,A61P25/16,A61P25/28,C12N5/10,C12Q1/48, PC
C12Q1/48,
PC      G01N33/15,G01N33/50,C12N15/00,C12N5/00
CC      Strandedness: Double;
CC      Topology: Linear;
CC      JNK3-Controller and method of using the same
FH      Key
FT      Location/Qualifiers
FEATURES
source
1..2366
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match
Best Local Similarity 97.7%; Score 82.8; DB 2; Length 2366;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      626 GTACCGAAGAGAGAGGCTGCTCTTACTACACCATTTTGTCTTTCTTCTGAATTC 685
DB      1478 GCACCTGAAGAGAGAGGCTGCTCTTACTACACCATTTTGTCTTTCTTCTGAATTC 1419
QY      686 ATTACTCTCTGTAGATTAAGTTCTGT 711
DB      1418 ATTACTCTCTGTAGATTAAGTTCTTT 1393

RESULT 21
AR16220/c
LOCUS      AR16220 2367 bp DNA linear PAT 07-OCT-2005
DEFINITION Sequence 3 from patent US 6943000.
ACCESSION AR16220
VERSION AR16220.1 GI:77364281
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2367)
AUTHORS Davis,R.J., Flavell,R.A., Rakic,P., Whitmarsh,A.J., Kuan,C.-Y. and Yang,D.D.
TITLE JNK3 modulators and methods of use
JOURNAL Patent: US 6943000-A 3 13-SEP-2005;
University of Massachusetts and Yale University, Boston, MA
FEATURES
source
1..2367
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match
Best Local Similarity 97.7%; Score 82.8; DB 2; Length 2367;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      626 GTACCGAAGAGAGAGGCTGCTCTTACTACACCATTTTGTCTTTCTTCTGAATTC 685
DB      1479 GCACCTGAAGAGAGAGGCTGCTCTTACTACACCATTTTGTCTTTCTTCTGAATTC 1420
QY      686 ATTACTCTCTGTAGATTAAGTTCTGT 711
DB      1419 ATTACTCTCTGTAGATTAAGTTCTTT 1394

```

```

RESULT 22
BC051731/c
LOCUS      BC051731 2494 bp mRNA linear PRI 06-OCT-2005
DEFINITION Homo sapiens mitogen-activated protein kinase 10, mRNA (cDNA clone MGC:50974 IMAGE:4838495), complete cds.
ACCESSION BC051731
VERSION BC051731.1 GI:30704986
KEYWORDS MGC.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 2494)
REFERENCE
1 (bases 1 to 2494)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diachenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramsen,R.D., Muijshy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Wortley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulik,S.W.,
Vitaliano,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahy,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchan,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schultz,J., Myers,R.M.,
Butterfield,Y.S., Krzywicki,M.I., Skalska,J., Smalins,D.E.,
Scherer,A., Schein,J.E., Jones,S.J. and Matra,M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2 (bases 1 to 2494)

JOURNAL PUBMED
REFERENCE
2 (bases 1 to 2494)
AUTHORS NIH MGC Project
CONSRTM Direct Submission
TITLE Submitted (01-MAY-2003) National Institutes of Health, Mammalian
JOURNAL Gene Collection (MGC), Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiroki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
Series: IRAC Plate: 90 Row: K Column: 24
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 20986509.
FEATURES
source
1..2494
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:50974 IMAGE:4838495"
/cisue_type="Testis"
/clone_1ib="NIH MGC_97"
/lab_host="DH10B"
/note="Vector: pBluecriptR"

```

```

gene
1. .2494
/ gene="MAPK10"
/ note="synonyms: P493F12, p54SAPK, JNK3A, FLJ12059, JNK3"
/ db_xref="GeneID:5602"
/ db_xref="GeneID:6872"
/ db_xref="HGNC:6872"
/ db_xref="IMGT/GENE-DB:6872"
/ db_xref="MIM:602897"
768..1727
/ gene="MAPK10"
/ codon_start=1
/ product="MAPK10 protein"
/ protein_id="AAH51731.1"
/ db_xref="GI:71297339"
/ db_xref="GeneID:5602"
/ db_xref="HGNC:6872"
/ db_xref="IMGT/GENE-DB:6872"
/ db_xref="MIM:602897"
/ translation="MEK1DANLCQVIMELDHMSYLLYQMLGKIHLSAGIIRH
LKSNIIVKSDCTLKIDFGIARTAGTSFMTFVYVRYRABEVLIGMGYKENVDM
SVGCIEMEMIKGAVLPRGTDIDOMNKVIEOLGCPGEPMKIOPTVRNVPKXA
GLTPPKLFPSPILPRADSEHNKLRASQARDLSKLVYDPAKRISVDALQPIYINWY
DPAVEAPPPQIIDKQIDEREHTLEEKELIYKVMNSEKTNVGVKQSPSGAAV
NSESLEPPSSVNDISSMSDQTLASPTDSLEASAGPLCCCR"

ORIGIN
Query Match 10.3%; Score 82.8; DB 5; Length 2494;
Best Local Similarity 97.7%; Pred. No. 3.7e-14;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGCTGCTCTTCTTACTACACCATTTTCTTCTTGAATTC 685
DB 1588 GCACCTGAAGAGAGAGCTGCTCTTCTTACTACACCATTTTCTTCTTGAATTC 1529
QY 686 ATTACTCTCTTGATAGATTCTGT 711
DB 1528 ATTACTCTCTTGATAGATTCTTT 1503

RESULT 23
AR454561/c
LOCUS AR454561
DEFINITION Sequence 34 from patent US 6682888.
ACCESSION AR454561
VERSION AR454561.1 GI:42688030
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2677)
AUTHORS Loring,J.F., Tingley,D.W. and Edwards,C.M.
TITLE Genes expressed in Alzheimer's disease
JOURNAL Patent: US 6682888-A 34 27-JAN-2004;
Incyte Corporation; Palo Alto, CA
FEATURES
source
1..2677
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 10.3%; Score 82.8; DB 2; Length 2677;
Best Local Similarity 97.7%; Pred. No. 3.7e-14;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGCTGCTCTTCTTACTACACCATTTTCTTCTTGAATTC 685
DB 1795 GCACCTGAAGAGAGAGCTGCTCTTCTTACTACACCATTTTCTTCTTGAATTC 1736
QY 686 ATTACTCTCTTGATAGATTCTGT 711
DB 1735 ATTACTCTCTTGATAGATTCTTT 1710

RESULT 24

```

```

BC022492/c
LOCUS BC022492
DEFINITION 2678 bp mRNA linear PRI 14-OCT-2004
HOMO sapiens mitogen-activated protein kinase 10, mRNA (cDNA clone
IMAGE:4792970).
ACCESSION BC022492
VERSION BC022492.1 GI:18490289
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 2678)
REFERENCE
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Scheaffer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heist,P.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Uedin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,
Mckernan,K.J., Malek,J.A., Gunatirane,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Huiyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahy,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Sklisa,V., Smalys,D.E.,
Scherer,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2678)
REFERENCE
AUTHORS Director MGC Project.
TITLE Direct Submission
JOURNAL Submitted (01-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
COMMENT NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiroki
Toshiyuki and Piero Carninci (RIKEN)
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Series: IRAX Plate: 32 Row: b Column: 8
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 20986504.
Location/Qualifiers
1..2678
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4792970"
/tissue_type="Brain, hypothalamus"
/clone_lib="NIH MGC_96"
/lab_host="DH10B"
/note="Vector: pBluescript"

ORIGIN

```

Query Match 10.3%; Score 82.8; DB 5; Length 2678;
 Best Local Similarity 97.7%; Pred. No. 3.7e-14;
 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGGCTGCTCTTCTTACTACACCATTTTCTTCTTCTGAAATTC 685
 |||||||
 DB 1775 GCACCTGAAGAGAGAGGCTGCTCTTCTTACTACACCATTTTCTTCTTCTGAAATTC 1716
 |||||||

QY 686 ATTACTCTCTGTAGATAGTCTGT 711
 |||||||

DB 1715 ATTACTCTCTGTAGATAGTCTGT 1690
 |||||||

RESULT 25
 BC035057/c 2690 bp mRNA linear PRI 03-AUG-2005
 LOCUS Homo sapiens mitogen-activated protein kinase 10, mRNA (cDNA clone
 DEFINITION MGC:41877 IMAGE:5261221), complete cds.
 ACCESSION BC035057
 VERSION BC035057.1 GI:71297045
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE
 1 (bases 1 to 2690)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, M.F., Rubin, G.M., Hong, L.,
 Scapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mallory, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hultk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Schevchenko, Y.,
 Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butlerfield, Y.S., Krzywinski, M.I., Skliska, U., Small, D.E.,
 Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Mammalian Gene Collection Program Team
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL
 PUBMED 12477932
 2 (bases 1 to 2690)

REFERENCE
 NIH MGC Project
 Direct Submission
 Submitted (31-JUL-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Bethesda, MD 20892-2550, USA
 NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 Contact: MGC help desk
 Email: cgabs-rt@mail.nih.gov
 cDNA Library Preparation: Miklos Palokovits, M.D., Ph.D.
 Tissue Procurement: Miklos Palokovits (NHGRI) & Shizaki
 Tohtiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 Contact: amadansystemsbiology.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

REMARK
 COMMENT
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>
 Series: IRAK Plate: 73 Row: d Column: 6
 This clone was selected for full length sequencing because it

FEATURES
 source
 passed the following selection criteria: matched mRNA gi: 20986509.
 Location/Qualifiers
 1..2690
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="MGC:41877 IMAGE:5261221"
 /issue_type="Brain, hippocampus"
 /clone_1fb="NIH MGC_95"
 /lab_host="DH10B"
 /note="Vector: pBluescript"

gene
 1..2690
 /gene="MAPK10"
 /note="synonyms: p493f12, p54bsAPK, JNK3A, FLJ12099, JNK3"
 /db_xref="GeneID:5602"
 /db_xref="MIM:602897"

CDS
 532..1926
 /gene="MAPK10"
 /codon_start=1
 /product="MAPK10 protein"
 /protein_id="AAH35057.1"
 /db_xref="GI:71297046"
 /db_xref="GeneID:5602"
 /db_xref="MIM:602897"
 /translation="MSLHPFLVYCSBPTLDVKIAFCGDFKQVDSYIAKHYMSKSYV
 DNPISVVGDSFTFVLKRYQNLKRGISGAGQIVCAAYDAVLDRAVALIKLSRPQNO
 THAKAYRELVMKVNHNKIIISLVNFTPQKTEEFQDVLVWELMDANLCOVOME
 LDHMSYLLVQMLGCIHLHSAQIHRDLKRSNTVVSDDTLKILDFGLARTAGTSF
 MNTPEVVRAPAVILMGYKENVDIWSVCGIEMVVRHKLFPGRDYIDQWVKVI
 BOLGPECEPKKLOPTRVYVKNPKYAGLTFPLPDSLPADSEHNKLKASQAD
 LLSKVLVDPKARISVDALQHPYINWVAPVAPVAPPOIYDKQLDDEEHTLEKE
 LIYKWNSEKTRNGVYKQSPBGAAVNSSESLPSSSVNDISMSIDQTLASDTD
 SLEASAPLGGCR"

ORIGIN
 Query Match 10.3%; Score 82.8; DB 5; Length 2690;
 Best Local Similarity 97.7%; Pred. No. 3.7e-14;
 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGCTCTTCTTACTACACCATTTTCTTCTTCTGAAATTC 685
 |||||||
 DB 1787 GCACCTGAAGAGAGGCTGCTCTTCTTACTACACCATTTTCTTCTTCTGAAATTC 1728
 |||||||

QY 686 ATTACTCTCTGTAGATAGTCTGT 711
 |||||||

DB 1727 ATTACTCTCTGTAGATAGTCTGT 1702
 |||||||

RESULT 26
 CS206710/c 2698 bp DNA linear PAT 08-DEC-2005
 LOCUS CS206710 Sequence 11 from Patent WO2005109001.
 DEFINITION CS206710
 ACCESSION CS206710
 VERSION CS206710.1 GI:83412265
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE
 1
 Spittaels, K.F.
 Patent: WO 2005109001-A 11 17-NOV-2005;
 Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
 Location/Qualifiers
 1..2698
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

FEATURES
 source
 ORIGIN
 Query Match 10.3%; Score 82.8; DB 2; Length 2698;
 Best Local Similarity 97.7%; Pred. No. 3.7e-14;

Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGGAGGCTGCTCTTACTACACCATTTTACTGCTTTCTTGCAATTC 685
 1810 GCACCTGAAGAGGAGGCTGCTCTTACTACACCATTTTACTGCTTTCTTGCAATTC 1751

Db 686 ATTACTCTCTTGATAGTACTGCTGT 711
 1750 ATTACTCTCTTGATAGTACTGCTGT 1725

RESULT 27
 AK124791 3081 bp mRNA linear PRI 20-JAN-2006
 LOCUS Homo sapiens cDNA FLJ42801 fis, clone BRCAN2001223, highly similar
 DEFINITION TO MITOGEN-ACTIVATED PROTEIN KINASE 10 (EC 2.7.1.-).

ACCESSION AK124791 GI:34530673
 VERSION AK124791.1
 KEYWORDS oligo capping; fis (full insert sequence).
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Makamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Ohtsuka, M., Nishitani, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagatani, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsura, N., Sato, K., Tanikawa, M., Yamazaki, M., Niimura, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hirooka, S., Chiba, Y., Ishida, S., Oho, Y., Takiguchi, S., Watanabe, S., Yoshida, M., Hoshino, T., Kusanagi, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T. O., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takouchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aocuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hiro, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Noguchi, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Saechi, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs Nat. Genet. 36 (1), 40-45 (2004)

JOURNAL PUBMED 14702039

REFERENCE 2
 Tanigami, A., Fujiwara, T., Shibahara, T., Goto, Y., Hirao, M., Shimizu, F., Wakebe, H., Ono, T., Hishigaki, H., Watanabe, T., Ozaki, K., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Makamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai, H., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahori, K., Masuho, Y., Nagai, K. and Isogai, T. NEDO human cDNA sequencing project unpublished

TITLE 3 (bases 1 to 3081)

JOURNAL Isogai, T. and Yamamoto, J.
 AUTHORS Direct Submission
 TITLES Submitted (15-JUL-2003) Takao Isogai, Helix Research Institute,

COMMENT

Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: flj-cdna@affy.com, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5' - 3' end one pass sequencing: RAB, HRI and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: Reverse Proteomics Research Institute, HRI and RAB.

FEATURES

source

1..3081
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="BRCAN2001223"
 /tissue_type="caudate nucleus"
 /clone_id="BRCAN2"
 /note="cloning vector: pME185FL3"

ORIGIN

Query Match 10.3%; Score 82.8; DB 5; Length 3081;
 Best Local Similarity 97.7%; Pred. No. 3.7e-14;
 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGGAGGCTGCTCTTACTACACCATTTTACTGCTTTCTTGCAATTC 685
 2194 GCACCTGAAGAGGAGGCTGCTCTTACTACACCATTTTACTGCTTTCTTGCAATTC 2135

Db 686 ATTACTCTCTTGATAGTACTGCTGT 711
 2134 ATTACTCTCTTGATAGTACTGCTGT 2109

RESULT 28
 AY888567 1269 bp mRNA linear SYN 22-MAR-2005
 LOCUS AY888567/c
 DEFINITION Synthetic construct Homo sapiens clone FLH17970.01X
 ACCESSION AY888567
 VERSION AY888567.1 GI:61358131
 KEYWORDS Human ORF Protect.
 SOURCE Synthetic construct
 ORGANISM Other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 1269)
 Hines, B., Halleck, A., Jepsen, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and Labaer, J. Cloning of human full-length cDNAs in Creator (TM) recombinational vector system

TITLE 2 (bases 1 to 1269)

JOURNAL Hines, B., Halleck, A., Jepsen, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and Labaer, J. Direct Submission
 Submitted (04-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA

COMMENT This cDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned with normalized stop-codon. The cDS has been directionally cloned using BD in-Fusion(TM) cloning system between the SalI and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence. Each clone is clonally isolated and full-length sequence-verified.

FEATURES

source

1..1269
 /organism="synthetic construct"
 /mol_type="mRNA"

/db_xref="taxon:32630"
 /clone="FLH117970.01X"
 /lab_host="Escherichia coli DH5alpha T1 resistant"
 /note="derived from Homo sapiens first strand cDNA library from placenta and brain"
 1. .1269
 /gene="MAPK10"
 1. .1269
 /gene="MAPK10"
 /codon_start=1
 /transl_table=11
 /product="mitogen-activated protein kinase 10"
 /protein_id="AAK41509.1"
 /db_xref="GI:61358132"
 /translation="MSLHLFLYCSPTLDVKIAFCGQFQKQVDVSYIAKHNNKSKV
 DNOFYSVEGDSFTFVLKRYONLKRIGSGAGQIVCAAYADLRNVAIKLSRPNQ
 THAKAYRELVLMKCVNHNKIISLVNFTFQKLEFQDYVILVMEIMDANLCQVIME
 LDHERMSYLLYOMLCGIIKHLHSAGIIRHDLKPSNIVVSDCTLKIDFGLARTAGTSF
 MMTPIVVTIRYRAPAVIIGMGYKENVDSVCGINGEMWRHKLIFPGRDYIDQWNV
 EQLGTCPEPFMKLQPTVRNRYENRKYAGLTFPKLPDLSLPADSEHNKLKASQARD
 LLSKMLVIDPAKRIISVDALQHPYINWYDPAVEAPPPQIYDKQLDEREHTIEWKE
 LIYKVMNSEKTKNGVVGQSPSAQVQO"

ORIGIN
 Query Match 10.1%; Score 80.4; DB 8; Length 1269;
 Best Local Similarity 98.8%; Pred. No. 2.2e-13;
 Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTGAATTCATTA 689
 |||||
 Db 1252 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTGAATTCATTA 1193
 |||||

QY 690 CTTCCTGTAGATAGTCTGT 711
 |||||
 Db 1192 CTTCCTGTAGATAGTCTTT 1171
 |||||

RESULT 29
 AY890997/c 1269 bp mRNA linear SYN 21-MAR-2005
 LOCUS Synthetic construct Homo sapiens clone FLH020610.01L
 DEFINITION mitogen-activated protein kinase 10 (MAPK10) mRNA, partial cds.
 ACCESSION AY890997
 KEYWORDS Human ORF Project.
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 1 (bases 1 to 1269)
 Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F.,
 Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
 Williamson, J. and Labaer, J.
 TITLE Cloning of human full-length CDS in Creator (TM) recombinational
 vector system
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1269)
 Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F.,
 Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
 Williamson, J. and Labaer, J.
 TITLE Direct Submission
 JOURNAL Submitted (05-JAN-2005) Biological Chemistry and Molecular
 Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
 Cambridge, MA 02141, USA
 COMMENT This CDS clone is a part of a collection of human full-length
 expression clones generated by Harvard Institute of Proteomics.
 This ORF clone has been cloned without stop-codon (to allow fusion
 with C-terminal tag). The CDS has been directionally cloned using
 BD In-Fusion (TM) cloning system between the SalI and HindIII sites
 of the pDNR-Dual vector. Additional sequences in the clone: 'ACC'
 after SalI site and before 'ATG' to provide Kozak consensus
 sequence; 'GG' after last codon and before HindIII site to maintain
 reading frame. Each clone is clonally isolated and full-length
 sequence-verified.

FEATURES
 source
 1. .1269
 /location/Qualifiers
 /mol_type="synthetic construct"
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /clone="FLH020610.01L"
 /lab_host="Escherichia coli DH5alpha T1 resistant"
 /note="derived from Homo sapiens first strand cDNA library from placenta and brain"
 1. .1269
 /gene="MAPK10"
 1. .1269
 /gene="MAPK10"
 /codon_start=1
 /transl_table=11
 /product="mitogen-activated protein kinase 10"
 /protein_id="AAK42931.1"
 /db_xref="GI:61366953"
 /translation="MSLHLFLYCSPTLDVKIAFCGQFQKQVDVSYIAKHNNKSKV
 DNOFYSVEGDSFTFVLKRYONLKRIGSGAGQIVCAAYADLRNVAIKLSRPNQ
 THAKAYRELVLMKCVNHNKIISLVNFTFQKLEFQDYVILVMEIMDANLCQVIME
 LDHERMSYLLYOMLCGIIKHLHSAGIIRHDLKPSNIVVSDCTLKIDFGLARTAGTSF
 MMTPIVVTIRYRAPAVIIGMGYKENVDSVCGINGEMWRHKLIFPGRDYIDQWNV
 EQLGTCPEPFMKLQPTVRNRYENRKYAGLTFPKLPDLSLPADSEHNKLKASQARD
 LLSKMLVIDPAKRIISVDALQHPYINWYDPAVEAPPPQIYDKQLDEREHTIEWKE
 LIYKVMNSEKTKNGVVGQSPSAQVQO"

ORIGIN
 Query Match 10.1%; Score 80.4; DB 8; Length 1269;
 Best Local Similarity 98.8%; Pred. No. 2.2e-13;
 Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTGAATTCATTA 689
 |||||
 Db 1252 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTGAATTCATTA 1193
 |||||

QY 690 CTTCCTGTAGATAGTCTGT 711
 |||||
 Db 1192 CTTCCTGTAGATAGTCTTT 1171
 |||||

RESULT 30
 AY891216/c 1269 bp mRNA linear SYN 21-MAR-2005
 LOCUS Synthetic construct Homo sapiens clone FLH117966.01L
 DEFINITION mitogen-activated protein kinase 10 (MAPK10) mRNA, partial cds.
 ACCESSION AY891216
 KEYWORDS Human ORF Project.
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 1 (bases 1 to 1269)
 Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F.,
 Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
 Williamson, J. and Labaer, J.
 TITLE Cloning of human full-length CDS in Creator (TM) recombinational
 vector system
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1269)
 Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F.,
 Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
 Williamson, J. and Labaer, J.
 TITLE Direct Submission
 JOURNAL Submitted (05-JAN-2005) Biological Chemistry and Molecular
 Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
 Cambridge, MA 02141, USA
 COMMENT This CDS clone is a part of a collection of human full-length
 expression clones generated by Harvard Institute of Proteomics.
 This ORF clone has been cloned without stop-codon (to allow fusion
 with C-terminal tag). The CDS has been directionally cloned using
 BD In-Fusion (TM) cloning system between the SalI and HindIII sites
 of the pDNR-Dual vector. Additional sequences in the clone: 'ACC'

after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Each clone is clonally isolated and full-length sequence-verified.

FEATURES

Location/Qualifiers
1..1269

/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/clone="FLH117965.01X"
/lab_host="Escherichia coli DH5alpha T1 resistant"
/note="derived from Homo sapiens first strand cDNA library from placenta and brain"

gene

CDS

1..>1269
/gene="MAPK10"
1..>1269
/gene="MAPK10"
/codon_start=1
/transl_table=11
/product="mitogen-activated protein kinase 10"
/protein_id="AA33143.1"
/db_xref="GI:61368268"
/translation="MSLHFLVYCSPTLDVKIAFCQGFQKQDVSYIAKYNNSKSKV
DNQFVSVEGDSFTFVLYKRYONLKPISGAGIYCAADAVLDNRVAIKLSRFPQNO
THAKAYRELVLAKCVNHNKIIISLVNFTPOKTLSEFQDYVLYMELMDANLCQVOME
LDHERMSYLYOMLCGKHLHSGIITHDLKPSNIVYKSDCTLKIIDPGLIARAGTSF
NMTPVYTRYRAPEVILGMYKENDVIVSGCINGEMVRHKLIFPGRIYIDQNKVI
EOLGTPCEPFMKKLOPTVRYNRYENRPRKATLTPFKLPDLSLPADSEHNKLKASQARD
LSKRLVIDPAKRISVDALQHPYINWVDPAEVAPPPQIYDKOLDEREHTIEWKE
LIVKWNSEKTKNGVVGKQSPSAQVOQ"

ORIGIN

Query Match 10.1%; Score 80.4; DB 8; Length 1269;
Best Local Similarity 98.8%; Pred. No. 2.2e-13;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTGAAATTCATTA 689

DB 1252 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTGAAATTCATTA 1193

QY 690 CTTCCCTTGATAGTCTGT 711

DB 1192 CTTCCCTTGATAGTCTGT 1171

RESULT 31
AY893302/c 1269 bp mRNA linear SYN 16-MAR-2005

LOCUS Synthetic construct Homo sapiens clone FLH057665.01X

DEFINITION mitogen-activated protein kinase 10 (MAPK10) mRNA, complete cds.

ACCESSION AY893302.1 GI:60815280

VERSION Human ORF Project.

KEYWORDS synthetic construct

SOURCE other sequences; artificial sequences.

ORGANISM 1 (bases 1 to 1269)

REFERENCE Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B.,

AUTHORS Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and Labaer, J.

TITLE Cloning of human full-length CDS FLEXGene in

JOURNAL Gateway (TM) recombinational vector system

COMMENT Unpublished

directionally cloned using the Gateway cloning system into pDONR 201. Additional sequences in the clone: 'ACC' before the 'ATG' (corresponding to ribosomal binding site and Kozak consensus sequences). Each clone is clonally isolated and full-length sequence-verified.

FEATURES

source

Location/Qualifiers
1..1269
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/clone="FLH057665.01X"
/lab_host="Escherichia coli DH5alpha T1 resistant"
/note="derived from Homo sapiens first strand cDNA library from placenta and brain"

gene

CDS

1..>1269
/gene="MAPK10"
1..>1269
/gene="MAPK10"
/codon_start=1
/transl_table=11
/product="mitogen-activated protein kinase 10"
/protein_id="AA33639.1"
/db_xref="GI:60815281"
/translation="MSLHFLVYCSPTLDVKIAFCQGFQKQDVSYIAKYNNSKSKV
DNQFVSVEGDSFTFVLYKRYONLKPISGAGIYCAADAVLDNRVAIKLSRFPQNO
THAKAYRELVLAKCVNHNKIIISLVNFTPOKTLSEFQDYVLYMELMDANLCQVOME
LDHERMSYLYOMLCGKHLHSGIITHDLKPSNIVYKSDCTLKIIDPGLIARAGTSF
NMTPVYTRYRAPEVILGMYKENDVIVSGCINGEMVRHKLIFPGRIYIDQNKVI
EOLGTPCEPFMKKLOPTVRYNRYENRPRKATLTPFKLPDLSLPADSEHNKLKASQARD
LSKRLVIDPAKRISVDALQHPYINWVDPAEVAPPPQIYDKOLDEREHTIEWKE
LIVKWNSEKTKNGVVGKQSPSAQVOQ"

ORIGIN

Query Match 10.1%; Score 80.4; DB 8; Length 1269;
Best Local Similarity 98.8%; Pred. No. 2.2e-13;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTGAAATTCATTA 689

DB 1252 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTGAAATTCATTA 1193

QY 690 CTTCCCTTGATAGTCTGT 711

DB 1192 CTTCCCTTGATAGTCTGT 1171

RESULT 32
AY893752/c 1269 bp mRNA linear SYN 16-MAR-2005

LOCUS Synthetic construct Homo sapiens clone FLH057664.01X

DEFINITION mitogen-activated protein kinase 10 (MAPK10) mRNA, partial cds.

ACCESSION AY893752.1 GI:60827196

VERSION Human ORF Project.

KEYWORDS synthetic construct

SOURCE other sequences; artificial sequences.

ORGANISM 1 (bases 1 to 1269)

REFERENCE Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B.,

AUTHORS Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and Labaer, J.

TITLE Cloning of human full-length CDS FLEXGene in

JOURNAL Gateway (TM) recombinational vector system

COMMENT Unpublished

This ORF clone has been cloned without stop-codon (to allow fusion

with C-terminal tag). After recombination sites have been added to either end of the ORF and directionally cloned using the Gateway cloning system into pDONR 201. Additional sequences in the clone: 'ACC' before the 'ATG' (corresponding to ribosomal binding site and Kozak consensus sequences). Each clone is clonally isolated and full-length sequence-verified.

FEATURES

Source

1..1269
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/clone="FLH057664.01L"
/lab_host="Escherichia coli DH5alpha T1 resistant"
/note="derived from Homo sapiens first strand cDNA library from placenta and brain"
1..>1269
/gene="MAPK10"
1..>1269
/gene="MAPK10"
/codon_start=1
/transl_table=11
/product="mitogen-activated protein kinase 10"
/protein_id="AA36789.1"
/db_xref="GI:60827197"
/translation="MSLHRYCYSEPTLDVKIAFCQGFQDKQVDVSYIAKHVNSKSV
DNOFYSVEGSDFTFLVKRYONLKPISGSAQIVCAAYDAVDNRVAIKLSRPFQNO
THAKRAYRELVLNKCVMNHKNIISLVNFTPOKLEEFQDYLVMELMDANLCOVIME
LDHERMSYLLYOMLCGIKHLHSAQIIRHDLKPSNIVKSDCTLKILDFGLATAGTSF
MNTPYVTVRYAPREVILGMVYKENVDMVSCICGEMVNRKILPFGRIADQMNVI
EOLGTPCEPFMKLOPTRYVYENRPNKAGLTFPKLPDPSLPADSEHNKLAQSQARD
LISKMLVIDPAKRISVDALOHPIYINWMDPAVEVAPPQIYDKQDEREHTIEWKE
LIYKVNNSSEKTRNGVVKGPSAQQVQOL"

CDS

ORIGIN

Query Match 10.1%; Score 80.4; DB 8; Length 1269;
Best Local Similarity 98.8%; Pred. No. 2.2e-13;

Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGCTGCTCTTTTACTACACATTTTGTCTTTCTTCTGAATTCATTA 669

DB 1252 CTGAAGAGAGAGCTGCTCTTTTACTACACATTTTGTCTTTCTTCTGAATTCATTA 1193

QY 690 CTTCCTTGTAGATTAAGTTCTGT 711

DB 1192 CTTCCTTGTAGATTAAGTTCTTT 1171

RESULT 33
BT019710/c 1269 bp mRNA linear SYN 28-OCT-2004

LOCUS BT019710 1269 bp mRNA linear SYN 28-OCT-2004

DEFINITION Synthetic construct Homo sapiens mitogen-activated protein kinase

10 mRNA, partial cds.

BT019710.1 GI:54696287

FLI CDNA.

SYNTHETIC CONSTRUCT

OTHER SEQUENCES; ARTIFICIAL SEQUENCES.

1 (bases 1 to 1269)

REFERENCE 1 (bases 1 to 1269)

AUTHORS Kalline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,

Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,

Phelan,M., and Farmer,A.

TITLE Cloning of human full-length CDSs in BD Creator(TM) System Donor

vector

Unpublished

2 (bases 1 to 1269)

REFERENCE 2 (bases 1 to 1269)

AUTHORS Kalline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,

Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,

Phelan,M., and Farmer,A.

TITLE Direct Submission

JOURNAL Submitted (28-OCT-2004) BD Biosciences Clontech, 1020 East Meadow

circle, Palo Alto, California 94303, USA

COMMENT This CDS clone is a part of a collection of human full length

expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the SalI and HindIII sites of the pDONR-DUAL vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: <http://bioinfo.clontech.com/orfclones>.

FEATURES

Source

1..1269
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/clone="GH01307L1.0"
/clone_1lb="BD Creator(TM) CDS Library derived from MGC collection"
/lab_host="DH5alpha T1 resistant"
/note="vector: pDONR-Dual"
1..>1269
/note="Mutations: 1268:Stop->L"
/codon_start=1
/transl_table=11
/product="mitogen-activated protein kinase 10"
/protein_id="AAV38516.1"
/db_xref="GI:54696288"
/translation="MSLHRYCYSEPTLDVKIAFCQGFQDKQVDVSYIAKHVNSKSV
DNOFYSVEGSDFTFLVKRYONLKPISGSAQIVCAAYDAVDNRVAIKLSRPFQNO
THAKRAYRELVLNKCVMNHKNIISLVNFTPOKLEEFQDYLVMELMDANLCOVIME
LDHERMSYLLYOMLCGIKHLHSAQIIRHDLKPSNIVKSDCTLKILDFGLATAGTSF
MNTPYVTVRYAPREVILGMVYKENVDMVSCICGEMVNRKILPFGRIADQMNVI
EOLGTPCEPFMKLOPTRYVYENRPNKAGLTFPKLPDPSLPADSEHNKLAQSQARD
LISKMLVIDPAKRISVDALOHPIYINWMDPAVEVAPPQIYDKQDEREHTIEWKE
LIYKVNNSSEKTRNGVVKGPSAQQVQOL"

CDS

ORIGIN

Query Match 10.1%; Score 80.4; DB 8; Length 1269;
Best Local Similarity 98.8%; Pred. No. 2.2e-13;

Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGCTGCTCTTTTACTACACATTTTGTCTTTCTTCTGAATTCATTA 669

DB 1252 CTGAAGAGAGAGCTGCTCTTTTACTACACATTTTGTCTTTCTTCTGAATTCATTA 1193

QY 690 CTTCCTTGTAGATTAAGTTCTGT 711

DB 1192 CTTCCTTGTAGATTAAGTTCTTT 1171

RESULT 34
BD249786/c 1306 bp DNA linear PAT 17-JUL-2003

LOCUS BD249786 1306 bp DNA linear PAT 17-JUL-2003

DEFINITION Polypeptides derived from JNK3.

BD249786.1 GI:33059556

KEYWORDS JP 2002534982-A/22.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homniidae; Homo

1 (bases 1 to 1306)

REFERENCE 1 (bases 1 to 1306)

AUTHORS Desanlis,F., Fournier,A., Maury,I. and Liu,O.Z.

TITLE Polypeptides derived from JNK3

JOURNAL Patent: JP 2002534982-A 22 22-OCT-2002;

AVENTIS PHARMA SA

OS Homo sapiens (human)

PN JP 2002534982-A/22

PD 22-OCT-2002

PF 19-JAN-2000 JP 2000594932

PR 20-JAN-1999 FR 99/00586, 26-FEB-1999 US 60/122175 PI

FRANCINE DESANLIS, ALAIN FOURNIER, ISABELLE MAURY, QING ZHOU LIU PC

C12N15/09, A61K39/395, A61K45/00, A61P7/10, A61P9/00, A61P25/00, PC

[illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	SOURCE
1	Hominidae; Homo.	Desanlis, F., Zhou-Liu, Q., Fournier, A. and Maury, I.			
		Polypeptides derived from jnk3			
		Patent: WO 0043524-A 22 27-JUL-2000;			
		AVANTIS PHARMA SA (FR) ; DESANLIS FRANÇINE (FR) ; ZHOU LIU QING (FR) ; FOURNIER ALAIN (FR) ; MAURY ISABELLE (FR)			
		Location/Qualifiers			
		1. .1306			
		/organism="Homo sapiens"			
		/mol_type="unassigned DNA"			
		/db_xref="taxon:9606"			
		142. .1296			
		/note="unnamed protein product"			
		/codon_start=1			
		/protein_id="CAC09125.1"			
		/db_xref="GI:10188270"			
		/translation="MSKSKVDNDFEYSEVSDSTFTVLYKRYONLKLIGSGAGIYCAAY			
		DAVIDELRVATIKLISRFQONTTHAKARATRELYLKKCVNKHITISLNFPTQKITEEQ			
		DVYLWELMDANLCQVIMELDHERNSYLLYOMLCGILKHLASGAIIRDLSPNIVAK			
		SDCTLKILDLGLARTAGTSPMTPEYVTRVYRAPEVLIGYKENVDIWSGCIJGEMSE			
		VRHETLPGRDYIDQWNVLEQGTPEPEMKLQPTVRNVVENRPYAGILTEPKLFP			
		DSLPADSEHNKIKASQARDLSMLYIDAKISYDDALOHPIYINWYDAEVEADPP			
		PQYDKDLDREHTIEEMKELIYKENVNSEKTKNGVYKQGPSAQVQ"			
Qy	630	CTGAAGAGAAAGGCTGCTCTTTACTACTACACCATTTTGTCTTTCTTGAATTCATTA	689		
Db	1279	CTGAAGAGAAAGGCTGCTCTTTACTACTACACCATTTTGTCTTTCTTGAATTCATTA	1220		
Qy	690	CTTCCTGTGATPAGTTCTGT	711		
Db	1219	CTTCCTGTGATPAGTTCTTT	1198		
RESULT 37.					
BD078046/c					
LOCUS	BD078046	1773 bp	DNA	linear	PAT 27-AUG-2002
DEFINITION	JNK3-controller and method of using the same.				
ACCESSION	BD078046				
VERSION	BD078046.1	GI:22623649			
KEYWORDS	JP 2001519146-A/3.				
SOURCE	unidentified				
ORGANISM	unclassified				
REFERENCE	unclassified sequences.				
AUTHORS	1 (bases 1 to 1773)				
REFERENCE	DAVIS, R.J., Flavell, R.A., Rakic, P., Whitmarsh, A.J., Kuan, C.Y. and				
TITLE	YANG, D.D.				
JOURNAL	JNK3-controller and method of using the same				
COMMENT	Patent: JP 2001519146-A 3 23-OCT-2001;				
	UNIVERSITY OF MASSACHUSETTS				
	OS Unidentified				
	PN JP 2001519146-A/3				
	PD 23-OCT-2001				
	PF 05-OCT-1998 JP 2000514991				
	PR 03-OCT-1997 US 60/060995				
	PI ROGER J DAVIS, RICHARD A FLAVELL, PASKO RAKIC, ALAN J WHITMARSH				
	PI, CHIA YIN KUAN,				
	PI, DERRI D YOUNG				
	PC C12N15/00, A01K67/027, A61K31/711, A61K45/00, A61K48/00, A61P9/10,				
	PC A61P21/00				
	PC A61P25/08, A61P25/14, A61P25/16, A61P25/28, C12N5/10, C12Q1/48, PC				
	C12Q1/68,				
	PC G01N33/15, G01N33/50, C12N15/00, C12N5/00				
	CC Strandedness: Double;				
	CC Topology: Linear;				
	CC JNK3-controller and method of using the same				
	FT Key Location/Qualifiers				
	1. .1773				
	FT source				

FEATURES FT
Location/Qualifiers
source 1.1773
/organism="Unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 10.1%; Score 80.4; DB 2; Length 1773;
Best Local Similarity 98.8%; Pred. No. 2.1e-13;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTCTTGAATTCATTA 689
1343 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTCTTGAATTCATTA 1284

Db 690 CTTCCTTGATAGTAAGTTCTGT 711
1283 CTTCCTTGATAGTAAGTTCTTT 1262

RESULT 38
COS92477/c 1773 bp DNA linear PAT 01-NOV-2004
LOCUS
DEFINITION Sequence 54 from Patent EP1469316.
ACCESSION COS92477
VERSION COS92477.1 GI:55165020
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Weihe,E.D., Schaefer,M.K., Gillen,C., Wetzel,I. and Wrendt,S.
TITLE Screening method
JOURNAL Patent: EP 1469316-A 54 20-OCT-2004;
Gruenenthal GmbH (DE)
FEATURES Location/Qualifiers
source 1.1773
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 10.1%; Score 80.4; DB 2; Length 1773;
Best Local Similarity 98.8%; Pred. No. 2.1e-13;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTCTTGAATTCATTA 689
1343 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTCTTGAATTCATTA 1284

Db 690 CTTCCTTGATAGTAAGTTCTGT 711
1283 CTTCCTTGATAGTAAGTTCTTT 1262

RESULT 39
AR716221/c 1773 bp DNA linear PAT 07-OCT-2005
LOCUS
DEFINITION Sequence 4 from patent US 6943000.
ACCESSION AR716221
VERSION AR716221.1 GI:77364282
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 1773)
Davis,R.J., Flavell,R.A., Rakic,P., Whitmarsh,A.J., Kuan,C.-Y. and Yang,D.D.
TITLE JNK3 modulators and methods of use
JOURNAL Patent: US 6943000-A 4 13-SEP-2005;

FEATURES University of Massachusetts and Yale University, Boston, MA
Location/Qualifiers
source 1.1773
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 10.1%; Score 80.4; DB 2; Length 1773;
Best Local Similarity 98.8%; Pred. No. 2.1e-13;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTCTTGAATTCATTA 689
1343 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTCTTGAATTCATTA 1284

Db 690 CTTCCTTGATAGTAAGTTCTGT 711
1283 CTTCCTTGATAGTAAGTTCTTT 1262

RESULT 40
AX377859/c 1773 bp DNA linear PAT 18-MAR-2002
LOCUS
DEFINITION Sequence 54 from Patent WO0212338.
ACCESSION AX377859
VERSION AX377859.1 GI:19573950
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Gillen,C., Wetzel,I., Wrendt,S., Weihe,E. and Schaefer,M.K.
TITLE Screening method
JOURNAL Patent: WO 0212338-A 54 14-FEB-2002;
Gruenenthal GmbH (DE)
FEATURES Location/Qualifiers
source 1.1773
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 10.1%; Score 80.4; DB 2; Length 1773;
Best Local Similarity 98.8%; Pred. No. 2.1e-13;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTCTTGAATTCATTA 689
1343 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTCTTGAATTCATTA 1284

Db 690 CTTCCTTGATAGTAAGTTCTGT 711
1283 CTTCCTTGATAGTAAGTTCTTT 1262

RESULT 41
HSU34820/c 1773 bp mRNA linear PRI 25-JUL-1996
LOCUS
DEFINITION Human JNK3 alpha1 protein kinase (JNK3A1) mRNA, complete cds.
ACCESSION U34820
VERSION U34820.1 GI:1463126
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 1773)
Gupta,S., Barrett,T., Whitmarsh,A.J., Cavanagh,J., Sluss,H.K., Derjard,B. and Davis,R.J.
TITLE Selective interaction of JNK protein kinase isoforms with

transcription factors
 JOURNAL EMBO J. 15 (11), 2760-2770 (1996)
 PUBMED 8654373
 REFERENCE 2 (bases 1 to 1773)
 AUTHORS Davis, R.J.
 TITLE Direct Submission
 JOURNAL Submitted (25-AUG-1995) Roger J. Davis, Molecular Medicine, University of Massachusetts Medical School, 373 Plantation Street, Worcester, MA 01605, USA
 COMMENT Derijard, B. Cell 76, 1025-1037, 1994
 Stuss, H. K. Mol. Cell. Biol. 14, 8376-8384, 1994.
 FEATURES
 source
 1. 1773
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /issue_type="brain"
 1. 1773
 /gene="JUNK3A1"
 92. 1360
 /gene="JUNK3A1"
 /note="JNK protein kinase isoform that phosphorylates the transcription factor C-Jun on Ser-63 and Ser-73"
 /product="1"
 /codon_start=1
 /protein_id="AAC50605.1"
 /db_xref="GI:1463127"
 /translation="MSLFLPYCYSEPTLDVKIAFCQGFQKQVDVSYIARHNSKSKV
 DNOFYSEVVDSTFTVLYKRYONLKPISGSGOGIVCAAYDAVLDNRVAIKKLSRPQNO
 THAKRAYRELIVLMKCVNHKIIISLNVFTFOKLEEFQVDVLYMEIMDNLCOVIME
 LDHERMSYLLQMLCGIKHLHSGIIRHDLKPSNTIVYKSDCTIKILDPGLARTGSF
 NMTPYVTVYRPAEYVILGKGYENVDISVGTIMEMRHKILFEGRPYIDOMNVI
 EQLGTCEPERMKLQPTKRYVNRKRIKGLTFPKLPSPSLFADSEHNKLUASQARD
 LISKMLVDPARKISVDALQHPYIVWYDPAVEAPPOIYDKOLDEREHTIEWKE
 LIYKEVMNSEKTRNGVXGQSPSPSAVOQ"

ORIGIN
 Query Match 10.1%; Score 80.4; DB 5; Length 1773;
 Best Local Similarity 98.8%; Pred. No. 2.1e-13;
 Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 630 CTGAAGAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTTCTGGAATTCATTA 689
 |||||
 DB 1343 CTGAAGAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTTCTGGAATTCATTA 1284
 |||||
 QY 690 CTTCTTGTAGATAAGTTCTGT 711
 |||||
 DB 1283 CTTCTTGTAGATAAGTTCTTT 1262
 |||||

RESULT 42
 CQ714411/c
 LOCUS CQ714411 2096 bp DNA linear PAT 03-FEB-2004
 DEFINITION Sequence 345 from Patent WO02068579.
 ACCESSION CQ714411
 VERSION CQ714411.1 GI:42275268
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1
 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
 Kite, such as nucleic acid arrays, comprising a majority of
 humenexons or transcripts, for detecting expression and other uses
 thereof
 Patent: WO 02068579-A 345 06-SBP-2002;
 JOURNAL PE Corporation (NY) (US)
 FEATURES
 source
 1. 2096
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"

ORIGIN /db_xref="taxon:9606"
 Query Match 10.1%; Score 80.4; DB 2; Length 2096;
 Best Local Similarity 98.8%; Pred. No. 2.1e-13;
 Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 630 CTGAAGAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTTCTGGAATTCATTA 689
 |||||
 DB 1199 CTGAAGAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTTCTGGAATTCATTA 1140
 |||||
 QY 690 CTTCTTGTAGATAAGTTCTGT 711
 |||||
 DB 1139 CTTCTTGTAGATAAGTTCTTT 1118
 |||||

RESULT 43
 AR709626/c
 LOCUS AR709626 2131 bp DNA linear PAT 21-SEP-2005
 DEFINITION Sequence 87 from patent US 6936450.
 ACCESSION AR709626
 VERSION AR709626.1 GI:76000136
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 2131)
 AUTHORS Levine, Z. and Bernstein, J.
 TITLE Variants of protein kinases
 JOURNAL Patent: US 6936450-A 87 30-AUG-2005;
 Compugen Ltd.; Tel Aviv;
 MOX;
 FEATURES
 source
 1. 2131
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN
 Query Match 10.1%; Score 80.4; DB 2; Length 2131;
 Best Local Similarity 98.8%; Pred. No. 2.1e-13;
 Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 630 CTGAAGAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTTCTGGAATTCATTA 689
 |||||
 DB 1225 CTGAAGAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTTCTGGAATTCATTA 1166
 |||||
 QY 690 CTTCTTGTAGATAAGTTCTGT 711
 |||||
 DB 1165 CTTCTTGTAGATAAGTTCTTT 1144
 |||||

RESULT 44
 CS206711/c
 LOCUS CS206711 2155 bp DNA linear PAT 08-DEC-2005
 DEFINITION Sequence 12 from Patent WO2005109001.
 ACCESSION CS206711
 VERSION CS206711.1 GI:83412266
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1
 Splittlaels, K.F.
 Patent: WO 2005109001-A 12 17-NOV-2005;
 Galapagos Genomics N.V. (BE); Splittlaels, Koenraad Frederick F. (BE)
 JOURNAL
 FEATURES
 source
 1. 2155
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match	Similarity	10.1%	Score 80.4	DB 2	Length 2155
Best Local	Similarity	98.8%	Pred. No. 2	le-13	
Matches	81	Conservative	0	Mismatches	1
				Indels	0
				Gaps	0
QY	630	CTGAAGGAGAAAGGCTGCTCTTTTACTACACCATTTTATGCTTTTCTTGATTCATTA	689		
DB	1258	CTGAAGGAGAAAGGCTGCTCTTTTACTACACCATTTTATGCTTTTCTTGATTCATTA	1199		
QY	650	CTTCCTGTAGTACTAGTCTGTG	711		
DB	1198	CTTCCTGTAGTACTAGTCTGTG	1177		
RESULT 45					
LOCUS	AK057723/c				
DEFINITION	Homo sapiens CDNA FLJ3161 f16, clone U78RU200517, highly similar to MITOGEN-ACTIVATED PROTEIN KINASE 10 (EC 2.7.1.-).				
ACCESSION	AK057723				
VERSION	AK057723.1				
KEYWORDS	oligo capping; f16 (full insert sequence).				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryotic Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Odayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahara, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosioki, T., Kaku, Y., Kodaira, N., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Nishimura, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoa, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hottura, T., Kusano, J., Togehara, K., Takahashi-Fujii, A., Hara, H., Tanase, T. O., Nomura, Y., Tagaya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Mutsaers, K., Yuuki, H., Osima, A., Sasaki, N., Aotsuka, S., Yoshioka, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terasahima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujisawa, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hiki, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Ohtani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsunaga, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togehashi, T., Oyama, M., Hara, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Saech, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuno, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isoqai, T. and Sugano, S.				
TITLE	Complete sequencing and characterization of 21,243 full-length human cDNAs				
JOURNAL	Nat. Genet. 36 (1), 40-45 (2004)				
PubMed	14702039				
REFERENCE	2				
AUTHORS	Suzuki, O., Sasaki, N., Aotsuka, S., Shoji, T., Ichihara, T., Shiohata, N., Matsunawa, K., Hirano, M., Sano, S., Nomura, R., Yoshioka, Y., Matsunaga, Y., Moriya, S., Chiba, E., Momiyama, H., Onogawa, S., Kaeriyama, S., Satoh, N., Watanabe, H., Takahashi, E., Katada, R., Kuga, N., Kuroda, A., Satoh, I., Kamata, K., Takami, S., Terasahima, Y., Watanabe, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai, H., O., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Osima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,				

TITLE	Negahari,K., Maunho,Y., Nagai,K. and Isegai,T.
JOURNAL	NEDO human cDNA sequencing project
REFERENCE	Unpublished
AUTHORS	Isegai,T., Otsuki,T. and Sugiyama,T.
JOURNAL	3 (bases 1 to 2156)
COMMENT	(bases 1 to 2156) Direct Submission Submitted (24-OCT-2001) Takao Isegai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:tlj-cdn@nifty.com, Tel:81-438-52-3975, Fax:81-438-52-3986) NEO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequenced: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.
FEATURES	Location/Qualifiers
Source	1..2156
	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="UTERU2000517"
	/tissue type="uterus"
	/clone_id="UTERU2"
	/note="Cloning vector: pME18SFL3"
ORIGIN	
Query Match	10.1%; Score 80.4; DB 5; Length 2156;
Best Local Similarity	98.8%; Pred. No.2,le-13;
Matches	81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	630 CTGAGAGAGAAGCGTGCTCTTTACTACACCATTATTTTGGTCCTTTCTTGCAATTCATTA 689
Db	1260 CTGAAGAGAGAGGCGTGCTCTTTACTACACCATTATTTTGGTCCTTTCTTGCAATTCATTA 1201
OY	690 CTTCCCTGTGATAGATTCTGT 711
Db	1200 CTTCTCTTGATAGATTCTTT 1179
RESULT 46	
BD078047/c	
LOCUS	BD078047 2372 bp DNA linear PAT 27-AUG-2002
DEFINITION	JNK3-controller and method of using the same.
ACCESSION	BD078047
VERSION	BD078047.1 GI:22623650
KEYWORDS	JP 2001519146-A/4.
SOURCE	unidentified
ORGANISM	unclassified
REFERENCE	unclassified sequences.
AUTHORS	1 (bases 1 to 2372)
TITLE	Davis,R.C., Flavell,R.A., Rakic,P., Whitmarsh,A.J., Kuan,C.Y. and
JOURNAL	Yang,D.D.
COMMENT	JNK3-controller and method of using the same Patent: JP 2001519146-A 4 23-OCT-2001; UNIVERSITY OF MASSACHUSETTS OS Unidentified PN JP 2001519146-A/4 PD 23-OCT-2001 PF 05-OCT-1998 JP 2000514991 PR 03-OCT-1997 US 60/060995 PI ROGER J DAVIS,RICHARD A FLAVELL,PASKO RAKIC,ALAN J WHITMARSH PI CHIA YIN KUAN, DERK DI YANG PC C1N15/09,A01K67/027,A61K31/711,A61K45/00,A61K48/00,A61P9/10, A61P21/00. PC A61P25/08,A61P25/14,A61P25/16,A61P25/28,C12N5/10,C12Q1/48, PC C12Q1/58, PC GO1N33/15,GO1N33/50,C12N15/00,C12N5/00 CC Topology: Linear; CC Strandedness: Double; CC JNK3-controller and method of using the same

	FEATURES	source	FT	Key	Location/Qualifiers
			FT	source	1..2372 /organism='Unidentified'.
					1..2372 /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"
	ORIGIN				
			Query Match	10.1%; Score 80.4; DB 2;	Length 2372;
			Best Local Similarity	98.8%; Pred. No. 2.1e-13;	
			Matches	81; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY			630	CTGAAGGAGAAGCGTGTCTTTACTACACCATTTTAAGTCTTTTCCTTGAAATTCATT	689
Db			1475	CTGAAGGAGAAGCGTGTCTTTACTACACCATTTTAAGTCTTTTCCTTGAAATTCATT	1416
OY			690	CTTCCTTGATGATAAGTTCTGT	711
Db			1415	CTTCCTTGATGATAAGTTCTTT	1394
RESULT 47					
LOCUS	BD078048/c				
DEFINITION	JNK3-controller and method of using the same.				
ACCSSION	BD078048				
VERSION	BD078048.1 GI:22623651				
KEYWORDS	JP 2001519146-A/5.				
SOURCE	unidentified				
ORGANISM	unclassified				
REFERENCE	unclassified sequences.				
AUTHORS	1 (bases 1 to 2372)				
	Davis,R.J., Flavell,R.A., Rakic,P., Whitmarsh,A.J., Kuan,C.Y. and Yang,D.D.				
TITLE	JNK3-controller and method of using the same				
JOURNAL	Patent: JP 2001519146-A 5 23-OCT-2001;				
COMMENT	UNIVERSITY OF MASSACHUSETTS				
	OS Unidentified				
	PN JP 2001519146-A/5				
	PD 23-OCT-2001				
	PF 05-OCT-1998 JP 2000514991				
	PR 03-OCT-1997 US 60/060995				
	PI ROGER J DAVIS,RICHARD A FLAVELL,PASKO RAKIC,ALAN J WHITMARSH				
	P1 ,CHIA YIN KUAN,				
	P1 DERK DI YANG				
	PC C12N15/09,A01K67/027,A61K31/711,A61K45/00,A61K48/00,A61P9/10,				
	PC A61P21/00,				
	PC A61P25/08,A61P25/14,A61P25/16,A61P25/28,C12N5/10,C12Q1/48, PC				
	C12Q1/68				
	PC G01N33/15,G01N33/50,C12N15/00,C12N5/00				
	CC Strandedness: Double;				
	CC Topology: Linear;				
	CC JNK3-controller and method of using the same				
	FH Key				
	FT Location/Qualifiers				
	1..2372				
	/organism='Unidentified'.				
	1..2372				
	/organism="unidentified"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:32644"				
ORIGIN					
			Query Match	10.1%; Score 80.4; DB 2;	Length 2372;
			Best Local Similarity	98.8%; Pred. No. 2.1e-13;	
			Matches	81; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY			630	CTGAAGGAGAAGCGTGTCTTTACTACACCATTTTAAGTCTTTTCCTTGAAATTCATT	689
Db			1475	CTGAAGGAGAAGCGTGTCTTTACTACACCATTTTAAGTCTTTTCCTTGAAATTCATT	1416

Query	Best Local Match	Score	Pred.	DB	Length	Indels	Gaps
630	CTGAAGAGAGGCTGCTCTTTTACTACACCATTTTCTTTCTTCTGAATTCATTA	10.1k	98.8k	DB 2	2372	0	0
1475	CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTCTTTCTTCTGAATTCATTA	10.1k	98.8k	DB 2	2372	0	0
690	CTTCTCTGTGATTAAGTTCTGT	10.1k	98.8k	DB 2	2372	0	0
1415	CTTCTCTGTGATTAAGTTCTGT	10.1k	98.8k	DB 2	2372	0	0
630	CTGAAGAGAGGCTGCTCTTTTACTACACCATTTTCTTTCTTCTGAATTCATTA	10.1k	98.8k	DB 2	2372	0	0
1475	CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTCTTTCTTCTGAATTCATTA	10.1k	98.8k	DB 2	2372	0	0
690	CTTCTCTGTGATTAAGTTCTGT	10.1k	98.8k	DB 2	2372	0	0
1415	CTTCTCTGTGATTAAGTTCTGT	10.1k	98.8k	DB 2	2372	0	0

Db 1415 CTTCCTGTGATAGTATGTTCTTT 1394

RESULT 50
AR716222/c 2372 bp DNA linear PAT 07-OCT-2005

LOCUS AR716222 Sequence 6 from patent US 6943000.

DEFINITION AR716222

ACCESSION AR716222

VERSION AR716222.1 GI:77364283

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2372)

AUTHORS Davis, R.J., Flavell, R.A., Rakic, P., Whitmarsh, A.J., Kuan, C.-Y. and Yang, D.D.

TITLE JNK3 modulators and methods of use

JOURNAL Patent: US 6943000-A 6 13-SEP-2005;

University of Massachusetts and Yale University; Boston, MA

FEATURES

Location/Qualifiers

1..2372

source

ORIGIN

Query Match 10.1%; Score 80.4; DB 2; Length 2372;

Best Local Similarity 98.8%; Pred. No. 2.1e-13;

Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAGGAGAGAGGCTGTCTTTACTACACCATTTTACTTTCTTCTTGAATTCATTA 689

Db 1475 CTGAGGAGAGAGGCTGTCTTTACTACACCATTTTACTTTCTTCTTGAATTCATTA 1416

QY 690 CTTCCTGTGATAGTATGTTCTTT 711

Db 1415 CTTCCTGTGATAGTATGTTCTTT 1394

Search completed: July 19, 2006, 20:10:46

Job time : 5076 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2006, 18:38:55 ; Search time 650 Seconds

(without alignments)
8581.229 Million cell updates/sec

Title: US10723681MOD.SEQ

Perfect score: 800
Sequence: 1.acattcttaaacctctta.....caataatacgtttgatg 800

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 524920 seqs, 3486124231 residues

-Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

N_Geneseq_8:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001as:*
- 5: Geneseq2001bs:*
- 6: Geneseq2002as:*
- 7: Geneseq2002bs:*
- 8: Geneseq2003as:*
- 9: Geneseq2003bs:*
- 10: Geneseq2003cs:*
- 11: Geneseq2003ds:*
- 12: Geneseq2004as:*
- 13: Geneseq2004bs:*
- 14: Geneseq2005s:*
- 15: Geneseq2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	798.4	99.8	76500	ADP45592 Human MAP
2	798.4	99.8	110950	ADP45592 Human MAP
3	463.4	57.9	823	ADY03500 Human mit
4	463.4	57.9	823	ADY03500 Human mit
5	82.8	10.3	1281	ABK50805 DNA encod
6	82.8	10.3	1422	AAA59380 DNA encod
7	82.8	10.3	1505	AAK37266 Nucleic a
8	82.8	10.3	1505	ABL88412 Pain regu
9	82.8	10.3	1505	AD131626 Human cDN
10	82.8	10.3	1505	AD131626 Human cDN
11	82.8	10.3	2211	AD583693 Human lym
12	82.8	10.3	2367	AD583693 Human lym
13	82.8	10.3	2677	AD583693 Human lym
14	82.8	10.3	2677	AD583693 Human lym
15	82.8	10.3	2677	AD583693 Human lym
16	80.4	10.1	972	AA593582 DNA encod
17	80.4	10.1	999	AA593582 DNA encod
18	80.4	10.1	1111	AA575684 DNA encod

19	80.4	10.1	1306	AA59379 DNA encod
20	80.4	10.1	1773	ABL88411 Pain regu
21	80.4	10.1	1773	ABL88411 Pain regu
22	80.4	10.1	1773	ABL88411 Pain regu
23	80.4	10.1	2155	AEQ09276 Human MAP
24	80.4	10.1	2372	AAK37266 Human MAP
25	80.4	10.1	2372	AAK37266 Human MAP
26	80.4	10.1	2372	AAK37266 Human MAP
27	80.4	10.1	2372	AAK37266 Human MAP
28	80.4	10.1	2372	AAK37266 Human MAP
29	80.4	10.1	2372	AAK37266 Human MAP
30	80.4	10.1	2372	AAK37266 Human MAP
31	80.4	10.1	2372	AAK37266 Human MAP
32	80.4	10.1	2372	AAK37266 Human MAP
33	80.4	10.1	2372	AAK37266 Human MAP
34	80.4	10.1	2372	AAK37266 Human MAP
35	80.4	10.1	2372	AAK37266 Human MAP
36	80.4	10.1	2372	AAK37266 Human MAP
37	80.4	10.1	2372	AAK37266 Human MAP
38	80.4	10.1	2372	AAK37266 Human MAP
39	80.4	10.1	2372	AAK37266 Human MAP
40	80.4	10.1	2372	AAK37266 Human MAP
41	80.4	10.1	2372	AAK37266 Human MAP
42	80.4	10.1	2372	AAK37266 Human MAP
43	80.4	10.1	2372	AAK37266 Human MAP
44	80.4	10.1	2372	AAK37266 Human MAP
45	80.4	10.1	2372	AAK37266 Human MAP
46	80.4	10.1	2372	AAK37266 Human MAP
47	80.4	10.1	2372	AAK37266 Human MAP
48	80.4	10.1	2372	AAK37266 Human MAP
49	80.4	10.1	2372	AAK37266 Human MAP
50	80.4	10.1	2372	AAK37266 Human MAP
51	80.4	10.1	2372	AAK37266 Human MAP
52	80.4	10.1	2372	AAK37266 Human MAP
53	80.4	10.1	2372	AAK37266 Human MAP
54	80.4	10.1	2372	AAK37266 Human MAP
55	80.4	10.1	2372	AAK37266 Human MAP
56	80.4	10.1	2372	AAK37266 Human MAP
57	80.4	10.1	2372	AAK37266 Human MAP
58	80.4	10.1	2372	AAK37266 Human MAP
59	80.4	10.1	2372	AAK37266 Human MAP
60	80.4	10.1	2372	AAK37266 Human MAP
61	80.4	10.1	2372	AAK37266 Human MAP
62	80.4	10.1	2372	AAK37266 Human MAP
63	80.4	10.1	2372	AAK37266 Human MAP
64	80.4	10.1	2372	AAK37266 Human MAP
65	80.4	10.1	2372	AAK37266 Human MAP
66	80.4	10.1	2372	AAK37266 Human MAP
67	80.4	10.1	2372	AAK37266 Human MAP
68	80.4	10.1	2372	AAK37266 Human MAP
69	80.4	10.1	2372	AAK37266 Human MAP
70	80.4	10.1	2372	AAK37266 Human MAP
71	80.4	10.1	2372	AAK37266 Human MAP
72	80.4	10.1	2372	AAK37266 Human MAP
73	80.4	10.1	2372	AAK37266 Human MAP
74	80.4	10.1	2372	AAK37266 Human MAP
75	80.4	10.1	2372	AAK37266 Human MAP
76	80.4	10.1	2372	AAK37266 Human MAP
77	80.4	10.1	2372	AAK37266 Human MAP
78	80.4	10.1	2372	AAK37266 Human MAP
79	80.4	10.1	2372	AAK37266 Human MAP
80	80.4	10.1	2372	AAK37266 Human MAP
81	80.4	10.1	2372	AAK37266 Human MAP
82	80.4	10.1	2372	AAK37266 Human MAP
83	80.4	10.1	2372	AAK37266 Human MAP
84	80.4	10.1	2372	AAK37266 Human MAP
85	80.4	10.1	2372	AAK37266 Human MAP
86	80.4	10.1	2372	AAK37266 Human MAP
87	80.4	10.1	2372	AAK37266 Human MAP
88	80.4	10.1	2372	AAK37266 Human MAP
89	80.4	10.1	2372	AAK37266 Human MAP
90	80.4	10.1	2372	AAK37266 Human MAP
91	80.4	10.1	2372	AAK37266 Human MAP

C 92	4	5.2	1412	10	ADJ64014	Ad3f4014 DNA seque
C 93	42	5.2	1418	2	AAO85308	Ad3f5308 UNK1 Onco
C 94	42	5.2	1418	2	AA485305	Ad4f5305 Human UNK
C 95	42	5.2	1418	6	AA148612	Ad148612 Human ins
C 96	42	5.2	1418	6	ABK83865	Human ins
C 97	42	5.2	1418	9	ADJ62607	Human CDN
C 98	42	5.2	1418	9	ADJ62307	CDNA enco
C 99	42	5.2	1418	9	ACA62748	Human C-J
C 100	42	5.2	1418	14	ADJ11993	Adj11993 Human Jun
	42	5.2	1418	14	AED33361	Ad333361 Human pro

ALIGNMENTS

RESULT 1	
ID ADP45592	standard; DNA; 76500 BP.
XX AC	ADP45592;
XX DT	26-AUG-2004 (first entry)
XX XX	Human MAP kinase MAPK10 (JNK3) gDNA.
DE KM	breast cancer; cytosolic; gene therapy; human; de; gene; SNP;
KM KM	single nucleotide polymorphism; MAP kinase; MAPK10; JNK3; p493F12;
KM KM	p54BAPK MAP kinase; c-Jun Kinase 3; JNK3 alpha protein kinase;
KM KM	c-Jun N-terminal kinase 3; stress activated protein kinase beta;
XX XX	chromosome 4q22.1-q23.
OS XX	Homo sapiens.
FH FH	Key Location/Qualifiers
FT FT	variation 191 /tag= a
FT FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT FT	variation 190 /tag= b
FT FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT FT	variation 3781 /tag= c
FT FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT FT	variation 3935 /tag= d
FT FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT FT	variation 4512 /tag= e
FT FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT FT	variation 7573 /tag= f
FT FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT FT	variation 8467 /tag= g
FT FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT FT	variation 9001 /tag= h
FT FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT FT	variation 9732 /tag= i
FT FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT FT	variation 13477 /tag= j
FT FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT FT	variation 13787 /tag= k
FT FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT FT	variation 13903 /tag= l
FT FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT FT	variation 14355 /tag= m
FT FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT FT	variation 15053 /tag= n
FT FT	/standard_name= "Single nucleotide polymorphism (SNP)"

FT	/tag= n	"Single nucleotide polymorphism (SNP) "
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	15459	
FT	/tag= o	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	17762	
FT	/tag= p	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	19482	
FT	/tag= q	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	19631	
FT	/tag= r	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	22170	
FT	/tag= s	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	22688	
FT	/tag= t	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	22748	
FT	/tag= u	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	23376	
FT	/tag= v	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	23826	
FT	/tag= w	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	23868	
FT	/tag= x	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	24154	
FT	/tag= y	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	25972	
FT	/tag= z	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	26057	
FT	/tag= aa	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	26361	
FT	/tag= ab	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	26599	
FT	/tag= ac	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	26712	
FT	/tag= ad	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	26812	
FT	/tag= ae	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	27069	
FT	/tag= af	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	32421	
FT	/tag= ag	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	33557	
FT	/tag= ah	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	35127	
FT	/tag= ai	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	35222	
FT	/tag= aj	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	35999	
FT	/tag= ak	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	36424	
FT	/tag= al	

PT		/standard_name=	"Single nucleotide polymorphism (SNP)"
FT	variation	37403	
FT		/*tag= am	
FT	variation	/standard_name=	"Single nucleotide polymorphism (SNP)"
FT		39203	
FT		/*tag= an	
FT	variation	/standard_name=	"Single nucleotide polymorphism (SNP)"
FT		39226	
FT		/*tag= ao	
FT	variation	/standard_name=	"Single nucleotide polymorphism (SNP)"
FT		41147	
FT		/*tag= ap	
FT	variation	/standard_name=	"Single nucleotide polymorphism (SNP)"
FT		46176	
FT		/*tag= aq	
FT	variation	/standard_name=	"Single nucleotide polymorphism (SNP)"
FT		50452	
FT		/*tag= ar	
FT	variation	/standard_name=	"Single nucleotide polymorphism (SNP)"
FT		52919	
FT		/*tag= as	
FT	variation	/standard_name=	"Single nucleotide polymorphism (SNP)"
FT		60214	
FT		/*tag= at	
FT	variation	/standard_name=	"Single nucleotide polymorphism (SNP)"
FT		61093	
FT		/*tag= au	
FT	variation	/standard_name=	"Single nucleotide polymorphism (SNP)"
FT		62572	
FT		/*tag= av	
FT	variation	/standard_name=	"Single nucleotide polymorphism (SNP)"
FT		63601	
FT		/*tag= aw	
FT	variation	/standard_name=	"Single nucleotide polymorphism (SNP)"
FT		65362	
FT		/*tag= ax	
FT	variation	/standard_name=	"Single nucleotide polymorphism (SNP)"
FT		65863	
FT		/*tag= ay	
FT	variation	/standard_name=	"Single nucleotide polymorphism (SNP)"
FT		66207	
FT		/*tag= az	
FT	variation	/standard_name=	"Single nucleotide polymorphism (SNP)"
FT		66339	
FT		/*tag= ba	
FT	variation	/standard_name=	"Single nucleotide polymorphism (SNP)"
FT		69512	
FT		/*tag= bb	
FT	variation	/standard_name=	"Single nucleotide polymorphism (SNP)"
FT		70759	
FT		/*tag= bc	
FT	variation	/standard_name=	"Single nucleotide polymorphism (SNP)"
FT		71217	
FT		/*tag= bd	
FT	variation	/standard_name=	"Single nucleotide polymorphism (SNP)"
FT		73382	
FT		/*tag= be	
FT	variation	/standard_name=	"Single nucleotide polymorphism (SNP)"
FT		76307	
FT		/*tag= bf	
FT	variation	/standard_name=	"Single nucleotide polymorphism (SNP)"
XX		WO2004047623-A2.	
XX		PD	
XX		10-JUN-2004.	
XX		PD	
PF	25-NOV-2003;	2003WO-US037948.	
XX			
PR	25-NOV-2002;	2002US-0429136F.	
PR	24-JUL-2003;	2003US-0490234F.	
Query Match	99.8%;	Score 796.4;	DB 12; Length 76500;
Similarity	99.9%;	Pred. No. 2.7e-171;	

[illegible]

```
KM Jun N terminal kinase-3; MAPK10.
XX Homo sapiens.
OS
FH Key
FT Location/Qualifiers
FT 206
FT /tag= a
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 1505
FT /tag= b
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 3796
FT /tag= c
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 3950
FT /tag= d
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 4527
FT /tag= e
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 7588
FT /tag= f
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 8482
FT /tag= g
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 9016
FT /tag= h
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 9018
FT /tag= i
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 9747
FT /tag= j
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 12207
FT /tag= k
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 13040
FT /tag= l
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 13492
FT /tag= m
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 13802
FT /tag= n
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 13918
FT /tag= o
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 14153
FT /tag= p
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 14370
FT /tag= q
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 15068
FT /tag= r
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 15474
FT /tag= s
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 17117
FT /tag= t
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 17777
FT /tag= u
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 19497
FT /tag= v
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 19646
FT /tag= w
FT variation
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 21751
FT /tag= x
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 22185
FT /tag= y
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 22703
FT /tag= z
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 22763
FT /tag= aa
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 23391
FT /tag= ab
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 23841
FT /tag= ac
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 23883
FT /tag= ad
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 24132
FT /tag= ae
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 24169
FT /tag= af
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 25987
FT /tag= ag
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 26072
FT /tag= ah
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 26376
FT /tag= ai
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 26614
FT /tag= aj
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 26727
FT /tag= ak
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 26827
FT /tag= al
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 27084
FT /tag= am
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 30965
FT /tag= an
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 32436
FT /tag= ao
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 32821
FT /tag= ap
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 32979
FT /tag= aq
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 33572
FT /tag= ar
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 35142
FT /tag= as
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 35237
FT /tag= at
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 36014
FT /tag= au
FT /standard_name= "Single nucleotide polymorphism (SNP)"
```

```

FT      variation      replace(36424,C)
FT      /*tag= av
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      36439
FT      variation      /*tag= aw
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      36838
FT      variation      /*tag= ax
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      36889
FT      variation      /*tag= ay
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      36839
FT      variation      /*tag= az
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      36857
FT      variation      /*tag= ba
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      36865
FT      variation      /*tag= bb
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      36885
FT      variation      /*tag= bc
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      38943
FT      variation      /*tag= bd
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      39035
FT      variation      /*tag= be
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      39046
FT      variation      /*tag= bf
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      39218
FT      variation      /*tag= bg
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      39241
FT      variation      /*tag= bh
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      40105
FT      variation      /*tag= bi
FT      /standard_name= "Single nucleotide polymorphism (SNP)"

Query Match      99.8%; Score 798.4; DB 14; Length 110950;
Best Local Similarity 99.9%; Pred. No. 2.9e-171;
Matches 799; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ACATTTTCTAAACCTTTATAGTGTGAGCATAGGCTTAGGAAAAATATATTAGCATT 60
DB      36016 ACATTTTCTAAACCTTTATAGTGTGAGCATAGGCTTAGGAAAAATATATTAGCATT 36075
QY      61 AATAAGTAATTTGTCTCAAGTCATCTAAAGCACATTACTAGGATCAGTAAAAATAAT 120
DB      36076 AATAAGTAATTTGTCTCAAGTCATCTAAAGCACATTACTAGGATCAGTAAAAATAAT 36135
QY      121 ATGACAAATTTGCTTGAATCTCTGCTGTACCAAGCAAAATTTTCCAGCTGACCTT 180
DB      36136 ATGACAAATTTGCTTGAATCTCTGCTGTACCAAGCAAAATTTTCCAGCTGACCTT 36195
QY      181 AACCGAGCCCATCTTGTAGATGTTTCAACTATTGTGCATCAACCTTGAGAAAGATTC 240
DB      36196 AACCGAGCCCATCTTGTAGATGTTTCAACTATTGTGCATCAACCTTGAGAAAGATTC 36255
QY      241 AAACACTAAGATGATGAGGAGAGAGGTAGCGGCTGAAAGATTACTGAGCTCCACATT 300
DB      36256 AAACACTAAGATGATGAGGAGAGAGGTAGCGGCTGAAAGATTACTGAGCTCCACATT 36315
QY      301 GACTTGATGCTCAAAAGGCAATTATGCTCTGAATTTTGATGAGGACACATTAACCTTTA 360
DB      36316 GACTTGATGCTCAAAAGGCAATTATGCTCTGAATTTTGATGAGGACACATTAACCTTTA 36375
QY      361 GCCCATGTTAACTTTCTTCAGATTCATTAATTAATTTATGAAAAAGTTT 420
DB      36376 GCCCATGTTAACTTTCTTCAGATTCATTAATTAATTTATGAAAAAGTTT 36435
QY      421 TGTCTGATCATTTACCATCAAGATATGATGATCCACACTGAATATCAAAAGAA 480
DB      36436 TGTCTGATCATTTACCATCAAGATATGATGATCCACACTGAATATCAAAAGAA 36495
QY      481 ATAAAACTAAATCAATTAATTAAGGACAAACCAATGATTTTGTGATCTGCTTTAAG 540
DB      36496 ATAAAACTAAATCAATTAATTAAGGACAAACCAATGATTTTGTGATCTGCTTTAAG 36555
QY      541 CAATGTTATGTTATTTCTTGCAACCCCTACACAAAGGCCAAGAAATTACACAAGTACTAG 600
DB      36556 CAATGTTATGTTATTTCTTGCAACCCCTACACAAAGGCCAAGAAATTACACAAGTACTAG 36615
QY      601 TTTATTTGTTATTCACGAGAGTGTACCTGTAAGAGAGAGGCTGCTTTTACTACACC 660
DB      36616 TTTATTTGTTATTCACGAGAGTGTACCTGTAAGAGAGAGGCTGCTTTTACTACACC 36675
QY      661 ATTTTATGCTTTTCTGCAATTCATTAATTCCTTTAGATTAAGTTGTTAAGAAACAG 720
DB      36676 ATTTTATGCTTTTCTGCAATTCATTAATTCCTTTAGATTAAGTTGTTAAGAAACAG 36735
QY      721 CTGTGTTATTAAGAAAACAAAATTTATCCTTCATCAGAGGAAATTCATTACTTAATGC 780
DB      36736 CTGTGTTATTAAGAAAACAAAATTTATCCTTCATCAGAGGAAATTCATTACTTAATGC 36795
QY      781 CAATTAATTAAGTTTGTATG 800
DB      36796 CAATTAATTAAGTTTGTATG 36815

RESULT 3
ADY03500
ID      ADY03500 standard; DNA; 823 BP.
XX
XX      ADY03500;
AC
XX
DT      05-MAY-2005 (first entry)
DE
XX      Human mitogen-activated protein kinase 10 SNP-containing gDNA MAPK10-AC.
XX
XX      SNP detection; breast tumor; endocrine disease;
XX      gynecology and obstetrics; neoplasm; cytostatic; metastasis;
XX      gene therapy; RNA interference; chromosome 4; ds; SNP;
XX      single nucleotide polymorphism; mitogen-activated protein kinase 10;
XX      Jun N terminal kinase-3; MAPK10.
OS      Homo sapiens.
FH
FT      Key      Location/Qualifiers
FT      variation      488
FT      /*tag= a
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX      WO2005014846-A2.
XX
XX      17-FEB-2005.
XX
XX      27-MAY-2004; 2004WO-US016939.
XX
XX      24-JUL-2003; 2003US-0490234P.
XX      25-NOV-2003; 2003US-00723681.
XX      25-NOV-2003; 2003US-0525239P.
XX
XX      (SECU-) SEQUENOM INC.
XX
XX      Rosh RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
XX      Hoyal-Wrightson CR;
XX
XX      WPI; 2005-163257/17.
XX
XX      Identifying risk of, preventing and/or treating breast cancer by
XX      identifying and/or analyzing polymorphic variations in nucleotide

```

PT sequences within the human genome.
XX
PS Example 17; Page 361; 617bp; English.
XX
CC The invention relates to a novel method for identifying a subject at risk
CC of breast cancer comprising detecting the presence or absence of a
CC polymorphic variation associated with breast cancer. The method of the
CC invention demonstrates cytosstatic activity and may be useful for
CC identifying a risk of, preventing and/or treating breast cancer and
CC cancer metastasis. The methods may be utilized for gene therapy or RNA
CC interference. The current sequence is that of the human mitogen-activated
CC protein kinase 10 (MAPK10) SNP-containing gDNA MAPK10-AC of the invention
CC which is located at chromosome 4q22.1-q23.
XX
SQ Sequence 823 BP; 277 A; 137 C; 113 G; 295 T; 0 U; 1 Other;
XX
Query Match 57.9%; Score 463.4; DB 14; Length 823;
Best Local Similarity 99.8%; Pred. No. 1.5e-95;
Matches 464; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 336 TTGTATGAGGACATTTACCCCTTAGCCCATGTTAACTTTCTTCAGATTCATTACTA 395
DB 1 TTGTATGAGGACATTTACCCCTTAGCCCATGTTAACTTTCTTCAGATTCATTACTA 60
QY 396 TTTAAATTATTTATGAAAAAGTTTGTCTGATCATTACCATCAGAAATATCAGAAATG 455
DB 61 TTTAAATTATTTATGAAAAAGTTTGTCTGATCATTACCATCAGAAATATCAGAAATG 120
QY 456 AATGCCACACTGAATATCAAAAGAAATTAATCAATCAATTTAAGGACACACCATGT 515
DB 121 AATGCCACACTGAATATCAAAAGAAATTAATCAATCAATTTAAGGACACACCATGT 180
QY 516 GATATTTGTTCATCTGCTCTTTAAGCAATGTTATGTTATTTCTTGAACCCCTACAA 575
DB 181 GATATTTGTTCATCTGCTCTTTAAGCAATGTTATGTTATTTCTTGAACCCCTACAA 240
QY 576 GGCAGAAATTCACAGATCAGTTATGTTATTTCAAGAGAGTGATGCTCGAAG 635
DB 241 GGCAGAAATTCACAGATCAGTTATGTTATTTCAAGAGAGTGATGCTCGAAG 300
QY 636 GAGAAAGCTGTCCTTTTACTACACCAATTTTACTCTTCTTGAATTCATTACTTCT 695
DB 301 GAGAAAGCTGTCCTTTTACTACACCAATTTTACTCTTCTTGAATTCATTACTTCT 360
QY 696 TGTAGATTAAGTTCTGTAGAAACAGCTGTGTATTTAAGAAAACAATTTATCTTCATC 755
DB 361 TGTAGATTAAGTTCTGTAGAAACAGCTGTGTATTTAAGAAAACAATTTATCTTCATC 420
QY 756 CACAGGAAATTCATTACTTAATGCCAAATTAATAGTTTGATG 800
DB 421 CACAGGAAATTCATTACTTAATGCCAAATTAATAGTTTGATG 465
XX
RESULT 4
ADY03501.
ID ADY03501 standard; DNA; 823 BP.
XX
AC ADY03501;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human mitogen-activated protein kinase 10 SNP-containing gDNA MAPK10-AD.
XX
KW SNP detection; breast tumor; endocrine disease;
KW gynecology and obstetrics; neoplasm; cytosstatic; metastasis;
KW gene therapy; RNA interference; chromosome 4; ds; SNP;
KW single nucleotide polymorphism; mitogen-activated protein kinase 10;
KW Jun N terminal kinase-3; MAPK10.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation 539

FT
FT /tag= a
XX /standard_name= "single nucleotide polymorphism (SNP)"
XX
PN MO2005014846-A2.
XX
PD 17-FEB-2005.
XX
PF 27-MAY-2004; 2004MO-US016939.
XX
PR 24-JUL-2003; 2003US-0490234P.
PR 25-NOV-2003; 2003US-00723681.
PR 25-NOV-2003; 2003US-0525239P.
XX
PA (SEQU-) SEQUENOM INC.
XX
PI Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
PI Hoyal-Wrightson CR;
XX
DR WPI; 2005-163257/17.
XX
XX
PT Identifying risk of, preventing and/or treating breast cancer by
PT identifying and/or analyzing polymorphic variations in nucleotide
PT sequences within the human genome.
XX
PS Example 17; Page 362; 617bp; English.
XX
CC The invention relates to a novel method for identifying a subject at risk
CC of breast cancer comprising detecting the presence or absence of a
CC polymorphic variation associated with breast cancer. The method of the
CC invention demonstrates cytosstatic activity and may be useful for
CC identifying a risk of, preventing and/or treating breast cancer and
CC cancer metastasis. The methods may be utilized for gene therapy or RNA
CC interference. The current sequence is that of the human mitogen-activated
CC protein kinase 10 (MAPK10) SNP-containing gDNA MAPK10-AD of the invention
CC which is located at chromosome 4q22.1-q23.
XX
SQ Sequence 823 BP; 278 A; 137 C; 112 G; 295 T; 0 U; 1 Other;
XX
Query Match 57.9%; Score 463.4; DB 14; Length 823;
Best Local Similarity 99.8%; Pred. No. 1.5e-95;
Matches 464; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 336 TTGTATGAGGACATTTACCCCTTAGCCCATGTTAACTTTCTTCAGATTCATTACTA 395
DB 1 TTGTATGAGGACATTTACCCCTTAGCCCATGTTAACTTTCTTCAGATTCATTACTA 60
QY 396 TTTAAATTATTTATGAAAAAGTTTGTCTGATCATTACCATCAGAAATATCAGAAATG 455
DB 61 TTTAAATTATTTATGAAAAAGTTTGTCTGATCATTACCATCAGAAATATCAGAAATG 120
QY 456 AATGCCACACTGAATATCAAAAGAAATTAATCAATCAATTTAAGGACACACCATGT 515
DB 121 AATGCCACACTGAATATCAAAAGAAATTAATCAATCAATTTAAGGACACACCATGT 180
QY 516 GATATTTGTTCATCTGCTCTTTAAGCAATGTTATGTTATTTCTTGAACCCCTACAA 575
DB 181 GATATTTGTTCATCTGCTCTTTAAGCAATGTTATGTTATTTCTTGAACCCCTACAA 240
QY 576 GGCAGAAATTCACAGATCAGTTATGTTATTTCAAGAGAGTGATGCTCGAAG 635
DB 241 GGCAGAAATTCACAGATCAGTTATGTTATTTCAAGAGAGTGATGCTCGAAG 300
QY 636 GAGAAAGCTGTCCTTTTACTACACCAATTTTACTCTTCTTGAATTCATTACTTCT 695
DB 301 GAGAAAGCTGTCCTTTTACTACACCAATTTTACTCTTCTTGAATTCATTACTTCT 360
QY 696 TGTAGATTAAGTTCTGTAGAAACAGCTGTGTATTTAAGAAAACAATTTATCTTCATC 755
DB 361 TGTAGATTAAGTTCTGTAGAAACAGCTGTGTATTTAAGAAAACAATTTATCTTCATC 420
QY 756 CACAGGAAATTCATTACTTAATGCCAAATTAATAGTTTGATG 800
DB 421 CACAGGAAATTCATTACTTAATGCCAAATTAATAGTTTGATG 465

```

RESULT 5
ABK50805/c
ID ABK50805 standard; DNA; 1281 BP.
XX
XX ABK50805;
XX
XX 30-JUL-2002 (first entry)
XX
XX DNA encoding recombinant stress-activated protein kinase b (SAPK b).
XX
XX Recombinant protein; stress-activated protein kinase b; SAPK b; gene; ds.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX FT 1.1281
XX CDS /*tag= a
XX FT /product= "SAPK b"
XX FT /note= "Recombinant stress-activated protein kinase b"
XX
XX KR9081424-A.
XX
XX PD 15-NOV-1999.
XX
XX PF 29-APR-1998; 98KR-00015362.
XX
XX PR 29-APR-1998; 98KR-00015362.
XX
XX PA (GLDS ) LG CHEM LTD.
XX
XX PI Park CG, Choo SH, Yoon HS, Chung HH;
XX
XX DR WPI; 2000-661807/64.
XX
XX DR P-PSDB; AAU79884.
XX
XX PT Process for preparing recombinant stress-activated protein kinase b (SAPK
XX PT b) using Escherichia coli.
XX
XX PS Disclosure; Fig 1; 9pp; Korean.
XX
XX CC The invention relates to a process for preparing recombinant stress-
XX CC activated protein kinase b (SAPK b) using Escherichia coli. This sequence
XX CC encodes a recombinant stress-activated protein kinase b associated
XX CC protein
XX
XX SQ Sequence 1281 BP; 390 A; 297 C; 305 G; 289 T; 0 U; 0 Other;

Query Match 10.3%; Score 82.8; DB 3; Length 1281;
Best Local Similarity 97.7%; Pred. No. 5.8e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGGAGCGTCCTTTACTACACCATTTTACTGCTTTCTTCTGAAATC 685
DB 1142 GCACCTGAAGAGGAGCGTCCTTTACTACACCATTTTACTGCTTTCTTCTGAAATC 1083
QY 686 ATTACTCTCTTGATTAAGTTCTGT 711
DB 1082 ATTACTCTCTTGATTAAGTTCTTT 1057

RESULT 6
AAK59380/c
ID AAK59380 standard; DNA; 1422 BP.
XX
XX AAK59380;
XX
XX 07-NOV-2000 (first entry)
XX
XX DNA encoding c-jun N-terminal kinase 3 derivative JNK3deltaNa1pha2.
XX
XX JNK3; c-jun N-terminal kinase 3; JNK3alpha1 isoform; JNK3alpha2 isoform;

```

```

XX mitogen-activated kinase; neurodegeneration; apoptosis; neuron;
XX neurodegenerative disease; Alzheimer's; Parkinson's; brain injury;
XX Huntington's disease; aging; acquired immune deficiency syndrome;
XX cerebral anoxia; hypoxia; edema; gene therapy; spinal cord injury;
XX retinal degeneration; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT 142.1422
XX CDS /*tag= a
XX FT /product= "JNK3deltaNa1pha2"
XX
XX PN MO200043524-A1.
XX
XX PD 27-JUL-2000.
XX
XX PF 19-JAN-2000; 2000WO-FR000104.
XX
XX PR 20-JAN-1999; 99FR-00000586.
XX
XX PR 26-FEB-1999; 99US-0122175P.
XX
XX PA (AVENTIS PHARMA SA.
XX
XX PI Desanlis F, Fournier A, Maury I, Zhou-Liu Q;
XX
XX DR WPI; 2000-499230/44.
XX
XX DR P-PSDB; AAB07789.
XX
XX PT New derivatives of c-jun N-terminal kinase 3, useful for identifying
XX PT ligands for treatment of neurodegeneration, have specific deletions from
XX PT known isoforms.
XX
XX PS Claim 10; Page 46-48; 57pp; French.
XX
XX CC The specification describes derivatives of JNK (c-jun N-terminal kinase)
XX CC 3, which have deletions from the N-terminal region corresponding to
XX CC positions 1-38 of the JNK3alpha1 and alpha2 isoforms or a C-terminal
XX CC deletion from position 139. JNK are mitogen-activated kinases implicated
XX CC in neurodegeneration and apoptosis of neurons. The derivatives are used
XX CC to identify specific ligands. These ligands, and JNK3-specific
XX CC antibodies, are used for prevention or treatment of neurodegenerative
XX CC diseases, e.g. Alzheimer's, Parkinson's or Huntington's diseases,
XX CC degeneration associated with aging or acquired immune deficiency
XX CC syndrome, brain injury, or cerebral anoxia, hypoxia or edema. Vector
XX CC containing sequences encoding the derivatives are useful in gene therapy,
XX CC e.g. of spinal cord injury and retinal degeneration. The present sequence
XX CC encodes the derivative JNK3deltaNa1pha2
XX
XX SQ Sequence 1422 BP; 436 A; 322 C; 329 G; 335 T; 0 U; 0 Other;

Query Match 10.3%; Score 82.8; DB 3; Length 1422;
Best Local Similarity 97.7%; Pred. No. 5.9e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGGAGCGTCCTTTACTACACCATTTTACTGCTTTCTTCTGAAATC 685
DB 1283 GCACCTGAAGAGGAGCGTCCTTTACTACACCATTTTACTGCTTTCTTCTGAAATC 1224
QY 686 ATTACTCTCTTGATTAAGTTCTGT 711
DB 1223 ATTACTCTCTTGATTAAGTTCTTT 1198

RESULT 7
AAK37266/c
ID AAK37266 standard; DNA; 1505 BP.
XX
XX AAK37266;
XX
XX 20-MAR-2003 (revised)
XX
XX DT 21-JUL-1999 (first entry)
XX

```


XX OS Homo sapiens.
XX PN US6607879-B1.
XX PD 19-AUG-2003.
XX PF 09-FEB-1998; 98US-00023655.
XX PR 09-FEB-1998; 98US-00023655.
XX PA (INCYTE) INCYTE CORP.
XX PI Cocks BG, Stuart SG, Seilhamer JU;
XX DR WPI; 2003-895307/82.
XX PT A composition comprising a plurality of cDNAs, useful for detecting
XX PT altered expression of genes in an immunological response or for
XX PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
XX PT or osteoarthritis.
XX PS Claim 1; SEQ ID NO 952; 50pp; English.
XX CC The invention relates to a composition comprising a plurality of cDNAs
XX CC for detecting the altered expression of genes in an immunological
XX CC response. The invention also relates to a method of diagnosing or
XX CC monitoring the treatment of an immunopathological condition in a sample,
XX CC comprising obtaining nucleic acids from a sample, contacting the nucleic
XX CC acids of the sample with an array comprising the plurality of cDNAs under
XX CC conditions to form one or more hybridisation complexes, detecting the
XX CC hybridisation complexes and comparing the levels of the detected
XX CC hybridisation complexes with the level of hybridisation complexes
XX CC detected in a non-diseased sample, where an altered level of the detected
XX CC hybridisation complexes correlates with the presence of an
XX CC immunopathological condition. Also disclosed are an expression profile
XX CC comprising a microarray and a plurality of detectable complexes and a
XX CC method for identifying a plurality of polynucleotide probes. The cDNAs
XX CC are useful as hybridisable array elements in a microarray for monitoring
XX CC the expression of target polynucleotides. The microarray can be used in
XX CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
XX CC ulcerative colitis, hypersensitization, irritable bowel syndrome,
XX CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
XX CC identifying agents for the treatment of the diseases. The microarray may
XX CC also be used in drug discovery and development, toxicological and
XX CC carcinogenicity studies, forensics or pharmacogenomics. The composition
XX CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
XX CC genomic fragments. This sequence represents a human cDNA of the
XX CC invention. Note: The sequence data for this patent did not form part of
XX CC the printed specification but was obtained in electronic format directly
XX CC from USPTO at seqdata.uspto.gov/sequence.html.
XX SQ Sequence 1505 BP; 459 A; 343 C; 346 G; 357 T; 0 U; 0 Other;
QY Query Match 10.3%; Score 82.8; DB 11; Length 1505;
DB Best Local Similarity 97.7%; Pred. No. 66-09; 2; Indels 0; Gaps 0;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GTACCTGAAGAGAGAGGCTGCTCTTTACTACACATTTTGTAGTCTTTCTTGAAATC 685
DB 1323 GCACCTGAAGAGAGAGGCTGCTCTTTACTACACATTTTGTAGTCTTTCTTGAAATC 1264
QY 686 ATTACTCTCTGTAGTAAGTTCTGT 711
DB 1263 ATTACTCTCTGTAGTAAGTTCTTT 1238
RESULT 10
AD883693/c
ID AD883693 standard; cDNA; 1505 BP.
AC AD883693;
XX

DT 11-AUG-2005 (first entry)
XX DE Human lymph node cDNA #952.
XX KW ss; gene; human; immunological response; blood cell; cancer;
XX KW immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis;
XX KW bronchitis; ulcerative colitis; diabetes; multiple sclerosis;
XX KW osteoporosis; pancreatitis; infection; arthritis; lymph node.
XX OS Homo sapiens.
XX PN US2004077003-A1.
XX PD 22-APR-2004.
XX PF 14-AUG-2003; 2003US-00641643.
XX PR 09-FEB-1998; 98US-00023655.
XX PA (INCYTE) INCYTE CORP.
XX PI Cocks BG, Stuart SG, Seilhamer JU;
XX DR WPI; 2004-387937/36.
XX PT New compositions having a number of first, second and third
XX PT polynucleotide probes, useful in research and diagnostic applications in
XX PT cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and
XX PT infections.
XX PS Claim 15; SEQ ID NO 952; 16pp; English.
XX CC The invention relates to polynucleotides which are used as probes to
XX CC detect genes differentially expressed in an immunological response,
XX CC abundantly expressed in an immunological response and/or coding for a
XX CC polypeptide known to regulate blood cell biology. The polynucleotides are
XX CC useful in research and diagnostic applications particularly in cancer and
XX CC immunopathological conditions, such as AIDS, allergies, anaemia, asthma,
XX CC atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple
XX CC sclerosis, osteoporosis, pancreatitis, infections and arthritis. The
XX CC present sequence represents a human lymph node cDNA used to detect blood
XX CC cell and immunological response gene expression. Note: The present
XX CC sequence does not appear in the printed specification but was obtained in
XX CC electronic format from the USPTO web site
XX CC (seqdata.uspto.gov/sequence.html?docid=20040077003).
XX SQ Sequence 1505 BP; 459 A; 343 C; 346 G; 357 T; 0 U; 0 Other;
QY Query Match 10.3%; Score 82.8; DB 13; Length 1505;
DB Best Local Similarity 97.7%; Pred. No. 66-09; 2; Indels 0; Gaps 0;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GTACCTGAAGAGAGAGGCTGCTCTTTACTACACATTTTGTAGTCTTTCTTGAAATC 685
DB 1323 GCACCTGAAGAGAGAGGCTGCTCTTTACTACACATTTTGTAGTCTTTCTTGAAATC 1264
QY 686 ATTACTCTCTGTAGTAAGTTCTGT 711
DB 1263 ATTACTCTCTGTAGTAAGTTCTTT 1238
RESULT 11
AEG09274/c
ID AEG09274 standard; DNA; 2211 BP.
AC AEG09274;
XX XX
XX 20-APR-2006 (first entry)
XX DE Human MAPK10, transcript variant 2 DNA.
XX KW amyloid-beta precursor protein; pharmaceutical;
XX KW mitogen activated protein-kinase inhibitor; neurological disease;
KW

XX Alzheimer's disease; degeneration; cognitive disorder; Neuroprotective;
KV Noctropic; substrate; mtogen-activated protein kinase 10; MAPK10; ds;
KW gene.
KM Homo sapiens.

OS
XX
XX Key Location/Qualifiers
FH 68..1462
FT CDS /*tag=a
FT /product= "mitogen-activated protein kinase 10 (MAPK10),
FT transcript variant 2"
TT

FN WO2005109001-A2.
PN
PP 17-NOV-2005.
PD
PE 12-MAY-2005; 2005WO-EP052182.
PF
PR 12-MAY-2004; 2004US-0570352P.
PX 24-AUG-2004; 2004US-0603948P.
PY

PA (GALA-) GALAPAGOS GENOMICS NV.
PB (LAEN/) LAENEN W.
PC
PD Spitzaele KF, Hoffmann M, Merchiers PG,
PE
PF MPI; 2006-231019/24.
PG P-PSDB; AEG09283.
PH REFSEQ; NM_138982.
PI

Pt Identifying a compound that inhibits amyloid-beta precursor protein
PT processing in a mammalian cell for treating e.g., Alzheimer's disease by
PT measuring a compound-polypeptide property related to amyloid-beta peptide
PT production.

Example 1; SEQ ID NO 10; 84pp; English.

This invention describes a novel method of identifying a compound that
inhibits the processing of amyloid-beta precursor protein in a mammalian
cell. The invention also describes: a) an agent for inhibiting amyloid-
beta precursor processing consisting of an antisense polynucleotide, a
ribozyme or a small interfering RNA (siRNA), where the agent comprises a
nucleic acid sequence complementary to, or engineered from, a naturally-
occurring polynucleotide sequence encoding the polypeptide comprising the
amino acid sequence of Aβ509278 or Aβ509279 and b) a pharmaceutical;
composition comprising the agent for inhibiting amyloid-beta precursor
processing or an amyloid-beta precursor processing-inhibiting amount of a
mtogen activated protein-kinase inhibitor in admixture with a carrier.
The method involves activation of a biological pathway producing an
indicator of the processing of amyloid-beta precursor protein e.g. a
phosphorylated substrate of a kinase comprising Aβ509266-Aβ509268. The
indicator induces the expression of a reporter e.g. alkaline phosphatase,
GFP, egfp, dGFP, luciferase or beta-galactosidase in the mammalian cell.
The pharmaceutical composition further comprises a label indicating use
of the composition for treating or preventing a condition involving
cognitive impairment or a susceptibility to the condition. The agent is
useful in the manufacture of a medicament for inhibiting the processing
or amyloid-beta precursor protein in a subject suffering from or
susceptible to the abnormal processing of the protein, or for treating or
preventing a condition involving cognitive impairment or a susceptibility
to the condition, preferably, Alzheimer's disease. This sequence encodes
human mtgen-activated protein kinase 10 (MAPK10), transcript variant 2,
a kinase involved in the up-regulation of amyloid-beta 1-42.

Sequence 2211 BP; 674 A; 498 C; 482 G; 557 T; 0 U; 0 Other;

Query Match 10.3%; Score 82.8; DB 15; Length 2211;
Best Local Similarity 97.7%; Pred. No. 6.5e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

626 GTACTGAAGAAGCGCTGTCTTTCATACCAATTGGTGCTTTCTTCGTGAATC 685
1323 GCACCTGAAAGGGAAGGCCTGTCTCTTTCCATAACAATTATTAAGTCTTTCTTCGAATTC 1266

Seq ID	Accession	Gene	Protein	Length	Score	DB	Length	Score	DB
1	AA037267	standard; DNA; 2367 BP.		2367	10.34	Score 82.8; DB 2;	Length 2367;		
2	AA037267	standard; DNA; 2367 BP.		2367	97.74	Pred. No. 6.6e-09;			
3	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
4	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
5	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
6	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
7	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
8	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
9	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
10	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
11	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
12	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
13	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
14	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
15	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
16	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
17	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
18	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
19	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
20	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
21	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
22	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
23	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
24	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
25	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
26	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
27	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
28	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
29	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
30	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
31	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
32	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
33	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
34	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
35	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
36	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
37	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
38	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
39	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	
40	AA037267	standard; DNA; 2367 BP.		2367	0;	Mismatches 2;	Indels 0;	Gaps 0;	

OY 686 ATTACTCTCTGTGATAGTTCNGT 711
 DB 1419 ATTACTCTCTGTGATAGTTCCTT 1394

RESULT 13
 ADI61666/c
 ID ADI61666 standard; cDNA, 2677 BP.

AC ADI61666;
 DE 22-APR-2004 (first entry)
 DE Human cDNA downregulated in Alzheimer's disease, INCYTE 413797.5.
 KW Human; ss; Alzheimer's disease; differential display; neuroprotective;
 KW brain disorder.
 XX Homo sapiens.
 XX US6682888-B1.
 PN 27-JAN-2004.
 PD 05-MAY-2000; 2000US-00566921.
 PF 05-MAY-2000; 2000US-00566921.
 PR 05-MAY-2000; 2000US-00566921.
 PA (INCY-) INCYTE CORP.
 PI Loring JF, Tingley DW, Edwards CM;
 DR WPI; 2004-118572/12.
 XX
 PT New composition comprising cDNAs that are differentially expressed in
 PT brain disorders, useful for diagnosing or treating Alzheimer's disease.
 XX
 PS Claim 1; SEQ ID NO 34; 223pp; English.

XX The invention relates to a new composition comprising ADI61633-
 CC ADI6170 and their complements that are cDNAs differentially expressed in
 CC brain disorders. Also included are a high throughput method for detecting
 CC differential expression of one or more cDNAs in a sample containing
 CC nucleic acids and a high throughput method for screening a library of
 CC molecules or compounds to identify a ligand that specifically binds a
 CC cDNA. The expression of the each of the cDNAs is downregulated at least
 CC two-fold in the brain of the subjects with Alzheimer's disease (ADI61727)
 CC ADI61727) or upregulated at least two fold in Alzheimer's disease
 CC (ADI61728-ADI61770). The composition is useful for diagnosing or treating
 CC Alzheimer's disease. The present sequence is a cDNA downregulated at
 CC least two-fold in the brain of the subjects with Alzheimer's disease.
 XX
 SQ Sequence 2677 BP; 785 A; 598 C; 581 G; 712 T; 0 U; 1 Other;

Query Match 10.3%; Score 82.8; DB 12; Length 2677;
 Best Local Similarity 97.7%; Pred. No. 6.8e-09;
 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 626 GTACCTGAGAGAGAGAGCTCTCTTTACTACACCAATTTTACTCTTTCTGCAATC 685
 DB 1795 GACACCGAGAGAGAGAGCTCTCTTTACTACACCAATTTTACTCTTTCTGCAATC 1736

OY 686 ATTACTCTCTGTGATAGTTCGT 711
 DB 1735 ATTACTCTCTGTGATAGTTCCTT 1710

RESULT 14
 AEA43831/c
 ID AEA43831 standard; cDNA, 2677 BP.
 AC AEA43831;

XX 25-AUG-2005 (first entry)
 DE Human cDNA differentially expressed in brain tissue SEQ ID NO:34.
 DE diagnosis; treatment; brain disease; neuroprotective; cerebroprotective;
 KW muscular-gen.; cytosolic; neuroleptic; nootropic; antidepressant;
 KW anticonvulsant; analgesic; antiparkinsonian; ophthalmological;
 KW immunotherapy; gene therapy; ss.
 XX Homo sapiens.
 OS US2005130171-A1.
 PN 16-JUN-2005.
 PD 26-JAN-2004; 2004US-00765700.
 PF 05-MAY-2000; 2000US-00566921.
 PR (INCY-) INCYTE CORP.
 PA Loring JF, Tingley DW, Edwards CM;
 PI WPI; 2005-456990/46.
 DR
 XX
 PT Composition useful for diagnosis, staging, treating or monitoring
 PT treatment of a subject with a brain disorder, comprises several cDNAs
 PT that are differentially expressed in brain disorders.
 XX
 PS Claim 1; SEQ ID NO 34; 231pp; English.

XX The invention relates to a composition (I) for the diagnosis, staging,
 CC treatment or for the monitoring of treatment of a subject with a brain
 CC disorder. (I) comprises several cDNAs that are differentially expressed
 CC in brain disorders and chosen from any one of 138 nucleotide sequences of
 CC AEA43798-AEA43935, or their complements. Also described: (1) a high
 CC throughput method for detecting differential expression of one or more
 CC cDNAs in a sample containing nucleic acids; (2) an isolated cDNA (II)
 CC selected from AEA43812, AEA43813, AEA43830, AEA43831, AEA43855, AEA43856,
 CC AEA43883 and AEA43923; (3) an expression vector (III) containing (II);
 CC (4) a host cell (IV) containing (III); (5) a protein (V) produced using
 CC (IV); and (6) a pharmaceutical composition comprising (V). (I) is useful
 CC for a high throughput method of screening a library of molecules or
 CC compounds to identify a ligand which specifically binds a cDNA, where the
 CC method involves combining (I) with the library of molecules or compound
 CC under conditions to allow specific binding and detecting specific binding
 CC between each cDNA and a molecule or compound. (IV) is useful for
 CC producing a protein, which involves culturing (IV) under conditions for
 CC the expression of the protein and recovering the protein from the
 CC culture. (V) is useful for high throughput method for screening a library
 CC of molecules or compounds to identify a ligand which specifically binds
 CC (V), where the method involves combining (V) or its portion with the
 CC library of molecules or compound under conditions to allow specific
 CC binding and detecting specific binding between (V) and a molecule or
 CC compound. (V) is useful for purifying a ligand from a sample, which
 CC involves combining (V) or its portion with the sample under conditions to
 CC allow specific binding, recovering the bound protein and separating the
 CC protein from ligand. (V) is also useful for producing an antibody, which
 CC involves immunizing an animal with (V) or its portion under conditions to
 CC elicit an antibody response, isolating animal antibodies and screening
 CC the isolated antibodies with the protein. (II) is useful in gene therapy
 CC for the treatment or prevention of conditions and disorders associated
 CC with immune response. The present sequence represents a human cDNA
 CC sequence which is differentially expressed in brain tissues, which is
 CC used in the exemplification of the present invention.
 XX

Sequence 2677 BP; 785 A; 598 C; 581 G; 712 T; 0 U; 1 Other;

Query Match 10.3%; Score 82.8; DB 14; Length 2677;
 Best Local Similarity 97.7%; Pred. No. 6.8e-09;
 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy		626GACCTCGAAGGAGGAGGGCTGTCTTTTACTACACCAATTTTAACTTCCTTGGAATC	689
Dd		1795GCACCTGGAAGGAGGAGGCTGTCTTTTACTACACCAATTTTAACTTCCTTGGAATC	1735
Oy		686ATTACTTCCTTGATAGTAAGTTCTGT	711
Dd		1735ATTACTTCCTTGATAGTAAGTTCTTT	1710
RESULT 15			
AEG09275/c			
ID		AEG09275 standard; DNA; 2698 BP.	
AC		AEG09275;	
DT		20-APR-2006 (first entry)	
XX			
XX		Human MAPK10, transcript variant 3 DNA.	
De			
KW		amyloid-beta precursor protein; pharmaceutical;	
KM		mitogen activated protein-kinase inhibitor; neurological disease;	
KM		Alzheimer's disease; degeneration; cognitive disorder; Neuroprotective;	
KM		Neurotropic; substrate; mitogen-activated protein kinase 10; MAPK10; de;	
KM		gene.	
OS		Homo sapiens.	
XX			
XX		Key location/Qualifiers	
Ft		CDS 669..1949	
Ft		/tag= a	
Ft		/product= "mitogen-activated protein kinase 10 (MAPK10),	
Ft		transcript variant 3"	
PV		MO2005109001-A2.	
XX			
PD		17-NOV-2005.	
XX			
PF		12-MAY-2005; 2005SWO-EP052182.	
PR		12-MAY-2004; 2004US-0570352P.	
PR		24-AUG-2004; 2004US-0603948P.	
PA		(GALA-) GALAPAGOS GENOMICS NV.	
PA		(LAEN/) LAENEN W.	
PI		Spliteaeis KF, Hoffmann M, Merchiers PG;	
DR		WPJ; 2006-231019/24.	
DR		P-PSDB; AEG09284.	
DR		REFSEQ; NM_138980.	
XX			
PT		Identifying a compound that inhibits amyloid-beta precursor protein	
PT		processing in a mammalian cell for treating e.g., Alzheimer's disease by	
PT		measuring a compound-polypeptide property related to amyloid-beta peptide	
PT		production.	
XX			
XX		Example 1; SEQ ID NO 11; 84pp; English.	
XX			
CC		This invention describes a novel method of identifying a compound that	
CC		inhibits the processing of amyloid-beta precursor protein in a mammalian	
CC		cell. The invention also describes: a) an agent for inhibiting amyloid-	
CC		-beta precursor processing consisting of an antisense polynucleotide; a	
CC		nucleic acid sequence complementary to, or engineered from, a naturally-	
CC		occurring polynucleotide sequence encoding the polypeptide comprising the	
CC		amino acid sequence of AEG09278 or AEG09279 and b) a pharmaceutical	
CC		composition comprising the agent for inhibiting amyloid-beta precursor	
CC		processing or an amyloid-beta precursor processing-inhibiting amount of a	
CC		mitogen activated protein-kinase inhibitor in admixture with a carrier.	
CC		The method involves activation of a biological pathway producing an	
CC		indicator of the processing of amyloid-beta precursor protein e.g., a	
CC		phosphorylated substrate of a kinase comprising AEG09266-AEG09268. The	
CC		indicator induces the expression of a reporter e.g. alkaline phosphatase,	

CC	GFP, eGFP, dGFP, Luciferase or beta-galactosidase in the mammalian cell.
CC	The pharmaceutical composition further comprises a label indicating use
CC	of the composition for treating or preventing a condition involving
CC	cognitive impairment or a susceptibility to the condition. The agent is
CC	useful in the manufacture of a medicament for inhibiting the processing
CC	of amyloid-beta precursor protein in a subject suffering from or
CC	susceptible to the abnormal processing of the protein, or for treating or
CC	preventing a condition involving cognitive impairment or a susceptibility
CC	to the condition, preferably, Alzheimer's disease. This sequence encodes
CC	human mitogen-activated protein kinase 10 (MAPK10), transcript variant 3,
CC	a kinase involved in the up-regulation of amyloid-beta 1-42.
SQ	Sequence 2698 BP; 792 A; 603 C; 585 G; 718 T; 0 U; 0 Other;
Query Match	10.3%; Score 82.8; DB 15; Length 2698;
Best Local Similarity	97.7%; Pred. No. 6.8e-09;
Matches 84; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
Oy	626 GTACCTTAAGAGAGAGCGTCGTCCCTTTACTACACACCATTATTTAGTCTTTCTTGCAATTC 685
Db	1810 GCACCTTAAGAGAGAGCGCTCCTTTACTACACCATTTTAGTCTTTCTTGCAATTC 1751
Oy	686 ATTAATCTTCCTTTGGTAGATAAGTTCTGT 711
Db	1750 ATTAATCTTCCTTTGGTAGATAAGTTCTTT 1725
RESULT 16	
AAS93582/C	
ID	AAS93582 standard; cDNA; 972 BP.
XX	AAS93582;
AC	
XX	13-FEB-2002 (first entry)
DT	
DE	DNA encoding novel human diagnostic protein #29386.
XX	
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;
XV	food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX	Homo sapiens.
XX	WO200175067-A2.
PN	
PD	11-OCT-2001.
XX	
PF	30-MAR-2001; 2001WO-US008631.
XX	
PR	31-MAR-2000; 2000US-00540217.
PR	23-AUG-2000; 2000US-00649167.
XX	
PA	(HYSE-) HYSBQ INC.
Pt	
PI	Drimac RT, Liu C, Tang YT;
XX	
DR	WPI: 2001-639362/73.
P-PSDB:	ABG29395.
PT	
PT	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity.
XX	
PS	Claim 1; SEQ ID NO 29386; 103bp; English.
XX	
CC	The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC	sequences. (I) is useful as hybridisation probes, polymerase chain
CC	reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC	and in recombinant production of (II). The polynucleotides are also used
CC	in diagnostics as expressed sequence tags for identifying expressed
CC	genes. (I) is useful in gene therapy techniques to restore normal
CC	activity of (II) or to treat disease states involving (II). (II) is
CC	useful for generating antibodies against it, detecting or quantitating a

CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 972 BP; 202 A; 268 C; 312 G; 190 T; 0 U; 0 Other;

Query Match 10.1%; Score 80.4; DB 5; Length 972;
Best Local Similarity 98.8%; Pred. No. 1.9e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 628 ACTGAGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTTCTTGAATTCAT 687
DB 453 AGCTGAGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTTCTTGAATTCAT 394
QY 688 TACTTCCTTGTAGATTAAGTTCT 709
DB 393 TACTTCCTTGTAGATTAAGTTCT 372

RESULT 17
AAS66964/c
ID AAS66964 standard; cDNA; 999 BP.
AC AAS66964;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #2768.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
XX OS
XX MO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX DR P-PSDB; ABG02777.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnosis, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX
XX Claim 1, SEQ ID NO 2768; 103bp; English.

XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal

CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 999 BP; 221 A; 277 C; 313 G; 188 T; 0 U; 0 Other;

Query Match 10.1%; Score 80.4; DB 5; Length 999;
Best Local Similarity 98.8%; Pred. No. 1.9e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 628 ACTGAGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTTCTTGAATTCAT 687
DB 453 AGCTGAGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTTCTTGAATTCAT 394
QY 688 TACTTCCTTGTAGATTAAGTTCT 709
DB 393 TACTTCCTTGTAGATTAAGTTCT 372

RESULT 18
AAS75684/c
ID AAS75684 standard; cDNA; 1111 BP.
AC AAS75684;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #11488.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
XX OS
XX MO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX DR P-PSDB; ABG11497.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnosis, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX
XX Claim 1, SEQ ID NO 11488; 103bp; English.

XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used

CC in diagnostic as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC XX

SQ Sequence 1111 BP; 224 A; 315 C; 356 G; 216 T; 0 U; 0 Other;

Query Match 10.1%; Score 80.4; DB 5; Length 1111;
Best Local Similarity 98.8%; Pred. No. 2e-08;

Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DY 628 ACCTGAAGAGGAGGCTGCTCTTTACTACACCTTTTGTGCTCTTCTTGATTCAT 687
DB 453 AGCTGAAGAGGAGGCTGCTCTTTACTACACCACTTTTGTGCTCTTCTTGATTCAT 394
DY 688 TACTCTCTGTAGTAAGTTCT 709
DB 393 TACTCTCTGTAGTAAGTTCT 372

RESULT 19

AAA59379/c
ID AAA59379 standard; DNA; 1306 BP.

XX AAA59379;

DT 07-NOV-2000 (first entry)

DE DNA encoding c-jun N-terminal kinase 3 derivative JNK3deltaNalpha1.

XX JNK3: c-jun N-terminal kinase 3; JNK3alpha1 isoform; JNK3alpha2 isoform;
XX mitogen-activated kinase; neurodegeneration; apoptosis; neuron;
XX neurodegenerative disease; Alzheimer's; Parkinson's; brain injury;
XX Huntington's disease; aging; acquired immune deficiency syndrome;
XX cerebral anoxia; hypoxia; edema; gene therapy; spinal cord injury;
XX retinal degeneration; ss.
XX

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 142..1296
XX /*tag= a
XX /product= "JNK3deltaNalpha1"

XX MO200043524-A1.

XX 27-JUL-2000.

XX 19-JAN-2000; 2000MO-FR000104.

XX 20-JAN-1999; 99FR-00000586.

XX 26-FEB-1999; 99US-0122175P.

XX (AVER) AVENTIS PHARMA SA.

XX Desanlis F, Fournier A, Maury I, Zhou-Liu Q;

XX WPI; 2000-499230/44.
XX P-PSDB; AAB07788.

PT New derivatives of c-jun N-terminal kinase 3, useful for identifying
PT ligands for treatment of neurodegeneration, have specific deletions from
PT known isoforms.
PT XX

XX Claim 10; Page 44-45; 57pp; French.

XX The specification describes derivatives of JNK (c-jun N-terminal kinase)
CC 3, which have deletions from the N-terminal region corresponding to
CC positions 1-38 of the JNK3alpha1 and alpha2 isoforms or a C-terminal
CC deletion from position 139. JNK are mitogen-activated kinases implicated
CC in neurodegeneration and apoptosis of neurons. The derivatives are used
CC to identify specific ligands. These ligands, and JNK3-specific
CC antibodies, are used for prevention or treatment of neurodegenerative
CC diseases, e.g. Alzheimer's, Parkinson's or Huntington's diseases,
CC degeneration associated with aging or acquired immune deficiency
CC syndrome, brain injury, or cerebral anoxia, hypoxia or edema. Vector
CC containing sequences encoding the derivatives are useful in gene therapy,
CC e.g. of spinal cord injury and retinal degeneration. The present sequence
CC encodes the derivative JNK3deltaNalpha1
CC XX

SQ Sequence 1306 BP; 415 A; 281 C; 301 G; 309 T; 0 U; 0 Other;

Query Match 10.1%; Score 80.4; DB 3; Length 1306;
Best Local Similarity 98.8%; Pred. No. 2e-08;

Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DY 630 CTGAAGAGGAGGCTGCTCTTTACTACACCACTTTTGTGCTCTTCTTGATTCATTA 689
DB 1279 CTGAAGAGGAGGCTGCTCTTTACTACACCACTTTTGTGCTCTTCTTGATTCATTA 1220
DY 690 CTTCCTGTAGTAAGTTCTGT 711
DB 1219 CTTCCTGTAGTAAGTTCTTT 1198

RESULT 20

ABL88411/c
ID ABL88411 standard; cDNA; 1773 BP.

XX ABL88411;

DT 16-MAY-2002 (first entry)

DE Pain regulated cDNA sequence 54.

XX Pain; analgesic; gene therapy; neurological disorder;
XX neurodegenerative disease; gene; ss.
XX
XX Homo sapiens.
XX

XX MO200212338-A2.

XX 14-FEB-2002.

XX 03-AUG-2001; 2001MO-EP009011.

XX 03-AUG-2000; 2000DE-01037759.

XX (CHEP) GRUENENTHAL GMBH.

XX Gillen C, Metzels I, Whendt S, Weihe E, Schaefer MK;

XX WPI; 2002-257469/30.

XX P-PSDB; ABB85006.

XX Identifying pain-regulating compounds, useful for treating chronic pain
XX and for diagnosis, by measuring binding of compounds to specific peptides
XX and proteins.

XX Claim 1; Fig 34; 213pp; German.

XX The invention relates to identifying pain-regulating substances (A)
CC comprises (i) incubating a test substance with a cell (or preparation

CC from (c) that has synthesized a peptide or protein (B) and (ii) measuring
CC either binding of the test substance to (B) or some functional parameter
CC that is altered by this binding. The method is useful for identifying
CC pain-regulating substances (A) with analgesic activity. (A) along with
CC nucleic acid (AB88411-AB88441) that encode proteins (B, AB885006-
CC AB885037) that interact with (A); (B); vectors containing the nucleic
CC acid; antibodies against (B); cells that express (B) and agents that bind
CC to (B), are all useful for treating pain, particularly chronic pain,
CC including use in gene therapy. The same materials can also be used for
CC diagnosis, e.g. of neurological and neurodegenerative diseases. The
CC present sequence is that of a polynucleotide of the invention
XX

SO Sequence 1773 BP; 555 A; 410 C; 388 G; 420 T; 0 U; 0 Other;
Query Match 10.1%; Score 80.4; DB 6; Length 1773;
Best Local Similarity 98.8%; Pred. No. 2.2e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAGAGAGAGGCTGCTCTTTTACTACACCATTTTATGCTTTCTTCTGAAATTCATTA 689
DB 1343 CTGAGAGAGAGAGGCTGCTCTTTTACTACACCATTTTATGCTTTCTTCTGAAATTCATTA 1284

QY 690 CTTCTCTTGATGATTAAGTTCTGT 711
DB 1283 CTTCTCTTGATGATTAAGTTCTTT 1262

RESULT 21
AED32365/c
ID AED32365 standard; DNA; 1773 BP.
XX
AC AED32365;
XX
DT 15-DEC-2005 (first entry)
XX
DE Human promyelocytic leukemia protein kinase encoding gene, SEQ ID 7.
XX
KM differentiation; cytosstatic; acute promyelocytic leukemia; gene; ds.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 92..1360
FT /*tag= a
FT /product= "Human promyelocytic leukemia protein kinase"
XX
PN JP2005281183-A.
XX
PD 13-OCT-2005.
XX
PF 29-MAR-2004; 2004JP-00097088.
XX
PR 29-MAR-2004; 2004JP-00097088.
XX
PA (KOKU-) KOKURITSU GAN CENT SOCHO.
XX
PA (DOKU-) DOKURITSU GYOSEI HOJIN IYAKUHIN IRYO KIK.
XX
PI Kitabayashi K;
XX
XX WPI; 2005-717904/74.
DR P-PSDB; AED32366.
XX
PT Differentiation inducing agent of leukemia cell useful as leukemia
PT therapeutic agent, comprises expression activator/functional activator of
PT promyelocytic leukemia protein, or expression inhibitor/functional
PT inhibitor of PMLK protein.
XX
PS Disclosure; SEQ ID NO 7; 28pp; Japanese.
XX
CC The invention relates to a novel differentiation inducing agent of a
CC leukemia cell. The agent comprises an expression activator or functional
CC activator of a promyelocytic leukemia (PML) protein, or an expression
CC inhibitor or functional inhibitor of the PML protein (a PML specific

CC protein phosphorylation enzyme). The invention further comprises a
CC screening method for the promyelocytic leukemia protein. The
CC differentiation inducing agent is useful as a therapeutic agent of
CC leukemia. This polynucleotide sequence represents the gene encoding a
CC human promyelocytic leukemia protein kinase (PMLK) of the invention.
XX

SO Sequence 1773 BP; 555 A; 410 C; 388 G; 420 T; 0 U; 0 Other;
Query Match 10.1%; Score 80.4; DB 14; Length 1773;
Best Local Similarity 98.8%; Pred. No. 2.2e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAGAGAGAGGCTGCTCTTTTACTACACCATTTTATGCTTTCTTCTGAAATTCATTA 689
DB 1343 CTGAGAGAGAGAGGCTGCTCTTTTACTACACCATTTTATGCTTTCTTCTGAAATTCATTA 1284

QY 690 CTTCTCTTGATGATTAAGTTCTGT 711
DB 1283 CTTCTCTTGATGATTAAGTTCTTT 1262

RESULT 22
AAS83445/c
ID AAS83445 standard; cDNA; 1872 BP.
XX
AC AAS83445;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #19249.
XX
KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
XX
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
PI WPI; 2001-639362/73.
DR P-PSDB; A8G19258.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
PS Claim 1; SEQ ID NO 19249; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1872 BP; 459 A; 499 C; 520 G; 394 T; 0 U; 0 Other;
Query Match 10.1%; Score 80.4; DB 5; Length 1872;
Best Local Similarity 98.8%; Pred. No. 2.2e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 628 ACCTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTGAAATTCAT 687
DB 453 AGCTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTGAAATTCAT 394
QY 688 TACTTCTCTGTAGTAAGTTCT 709
DB 393 TACTTCTCTGTAGTAAGTTCT 372
RESULT 23
ID AEG09276/C
XX AEG09276 standard; DNA; 2155 BP.
AC AEG09276;
XX
DT 20-APR-2006 (first entry)
XX
DE Human MAPK10, transcript variant 4 DNA.
XX
XX amyloid-beta precursor protein; pharmaceutical;
KM mtogen activated protein-kinase inhibitor; neurological disease;
KM Alzheimer's disease; degeneration; cognitive disorder; Neuroprotective;
KM Neurotropic; substrate; mtogen-activated protein kinase 10; MAPK10; de;
KM gene.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 442..1275
FT /tag= a
FT /product= "mtogen-activated protein kinase 10 (MAPK10),
FT transcript variant 4"
XX
XX MO2005109001-A2.
XX
XX
PD 17-NOV-2005.
XX
XX
PF 12-MAY-2005; 2005MO-EP052182.
XX
XX 12-MAY-2004; 2004US-0570352P.
XX
PR 24-AUG-2004; 2004US-0603948P.
XX
XX (GALA-) GALAPAGOS GENOMICS NV.
XX
XX (LAEN/) LAENEN W.
XX
XX
XX Splitteale KF, Hoffmann M, Merchiers PG;
XX
XX
XX WPI; 2006-231019/24.
XX
XX P-PDB; AEG09285.
XX
XX REFSQ; NM_138981.
XX
XX
XX Identifying a compound that inhibits amyloid-beta precursor protein
XX processing in a mammalian cell for treating e.g., Alzheimer's disease by
XX measuring a compound-polypeptide property related to amyloid-beta peptide
XX production.
XX
XX Example 1; SEQ ID NO 12; 84bp; English.
XX
XX This invention describes a novel method of identifying a compound that

CC inhibits the processing of amyloid-beta precursor protein in a mammalian
CC cell. The invention also describes; a) an agent for inhibiting amyloid-
CC beta precursor processing consisting of an antisense polynucleotide, a
CC ribozyme or a small interfering RNA (siRNA), where the agent comprises a
CC nucleic acid sequence complementary to, or engineered from, a naturally-
CC occurring polynucleotide sequence encoding the polypeptide comprising the
CC amino acid sequence of AEG09276 or AEG09279 and b) a pharmaceutical
CC composition comprising the agent for inhibiting amyloid-beta precursor
CC processing or an amyloid-beta precursor processing-inhibiting amount of a
CC mtogen activated protein-kinase inhibitor in admixture with a carrier.
CC The method involves activation of a biological pathway producing an
CC indicator of the processing of amyloid-beta precursor protein e.g. a
CC phosphorylated substrate of a kinase comprising AEG09266-AEG09268. The
CC indicator induces the expression of a reporter e.g. alkaline phosphatase,
CC GFP, eGFP, dGFP, luciferase or beta-galactosidase in the mammalian cell.
CC The pharmaceutical composition further comprises a label indicating use
CC of the composition for treating or preventing a condition involving
CC cognitive impairment or a susceptibility to the condition. The agent is
CC useful in the manufacture of a medicament for inhibiting the processing
CC of amyloid-beta precursor protein in a subject suffering from or
CC susceptible to the abnormal processing of the protein, or for treating or
CC preventing a condition involving cognitive impairment or a susceptibility
CC to the condition, preferably, Alzheimer's disease. This sequence encodes
CC human mtogen-activated protein kinase 10 (MAPK10), transcript variant 4,
CC a kinase involved in the up-regulation of amyloid-beta 1-42.
XX
XX
SQ Sequence 2155 BP; 629 A; 508 C; 446 G; 572 T; 0 U; 0 Other;
Query Match 10.1%; Score 80.4; DB 15; Length 2155;
Best Local Similarity 98.8%; Pred. No. 2.3e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 630 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTGAAATTCATTA 689
DB 1258 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTGAAATTCATTA 1199
QY 690 CTTCCTGTAGTAAGTTCTGT 711
DB 1198 CTTCCTGTAGTAAGTTCTTT 1177
RESULT 24
ID AAX37276/C
XX AAX37276 standard; DNA; 2372 BP.
AC AAX37276;
XX
XX
XX 20-MAR-2003 (revised)
XX
XX 21-JUL-1999 (first entry)
XX
XX
XX Seq ID No: 6 of WO9918193.
XX
XX
XX C-Jun N-terminal kinase 3; JNK3; transgene; excitotoxicity; disorder;
XX Alzheimer's disease; Huntington disease; amyotrophic lateral sclerosis;
XX ischemia; trauma; motorneuron disease; Parkinson's disease; epilepsy;
XX human; ss.
XX
XX
XX Homo sapiens.
XX
XX
XX MO9918193-A1.
XX
XX
XX 15-APR-1999.
XX
XX
XX 05-OCT-1998; 98WO-US020904.
XX
XX
XX 03-OCT-1997; 97US-0060995P.
XX
XX (UYMA-) UNIV MASSACHUSETTS.
XX
XX
XX Davis RJ, Flavell RA, Rakic P, Whitmarsh AJ, Kuan C, Yang D;
XX
XX WPI; 1999-287734/27.
XX
XX

FT Identification of c-Jun N-terminal kinase 3 modulators.
XX
PS Disclosure; Fig 2D; 88pp; English.
XX
CC The invention relates to a method for identifying compounds that modulate
CC c-Jun N-terminal kinase 3 (JNK3) expression or activity. The method
CC comprises (a) incubating a cell that can express a JNK3 protein, or that
CC has JNK3 activity, with a compound under conditions and for a time
CC sufficient for the cell to express a JNK3 protein/activity without the
CC compound; (b) incubating a control cell under the same conditions and for
CC the same time without the compound; (c) measuring JNK3 expression and
CC activity in the cell in the presence of the compound; (d) comparing the
CC amount of JNK3 expression/activity in the presence and absence of the
CC compound, where a difference in the level of expression/activity
CC indicates that the compound modulates JNK3 expression/activity. The
CC invention also provides a transgenic non-human mammal having a transgene
CC disrupting expression of a JNK3 gene, the transgene being chromosomally
CC integrated into germ cells of the mammal. JNK3 expression inhibitors,
CC e.g. antisense nucleic acids, are used to treat disorders involving
CC excitotoxicity, e.g. Alzheimer's disease, Huntington disease, ischemia,
CC amyotrophic lateral sclerosis, trauma, motor neuron disease, Parkinson's
CC disease or epilepsy. JNK3 sequences under Genbank accession numbers
CC U34819, U34820, U07620, L27128, U35236, X12740 and V00727 can be used in
CC the method of the invention. (Updated on 20-MAR-2003 to correct DR
CC field.)
XX
SQ Sequence 2372 BP; 714 A; 548 C; 519 G; 591 T; 0 U; 0 Other;
XX
Query Match 10.1%; Score 80.4; DB 2; Length 2372;
Best Local Similarity 98.8%; Pred. No. 2.3e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 630 CTGAAGAGAGAGCGTCTCTTCTACACACATTTTACCTTTCTTCTGAATTCATTA 689
DB 1475 CTGAAGAGAGAGCGTCTCTTCTTACTACACCATTTTACCTTTCTTCTGAATTCATTA 1416
CTTCTCTGTAGATTAAGTTCTGT 711
QY 690
DB 1415 CTTCTCTGTAGATTAAGTTCTTT 1394
CTTCTCTGTAGATTAAGTTCTTT 1394
XX
RESULT 25
AAL48611/c
XX AAL48611 standard; cDNA; 2372 BP.
XX
AC AAL48611;
XX
DT 11-OCT-2002 (first entry)
XX
DE Human insulin receptor signaling modifier cDNA SEQ ID NO: 5.
XX
KW Human; insulin receptor signaling; insulin receptor signaling modifier;
XX ISM; diabetes; metabolic syndrome; antidiabetic; gene; ss.
XX
OS Homo sapiens.
XX
PN MO200255664-A2.
XX
PD 18-JUL-2002.
XX
PF 11-JAN-2002; 2002MO-US001048.
XX
PR 12-JAN-2001; 2001US-0261326P.
PR 12-JAN-2001; 2001US-0261303P.
PR 12-JAN-2001; 2001US-0261304P.
PR 12-JAN-2001; 2001US-0261335P.
PR 12-JAN-2001; 2001US-0261336P.
PR 12-JAN-2001; 2001US-0261361P.
PR 12-JAN-2001; 2001US-0261456P.
PR 12-JAN-2001; 2001US-0261457P.
PR 12-JAN-2001; 2001US-0261458P.
PR 12-JAN-2001; 2001US-0261459P.
PR 12-JAN-2001; 2001US-0261461P.

PR 12-JAN-2001; 2001US-0261518P.
PR 12-JAN-2001; 2001US-0261531P.
PR 12-JAN-2001; 2001US-0261532P.
PR 12-JAN-2001; 2001US-0261589P.
PR 12-JAN-2001; 2001US-0261590P.
PR 12-JAN-2001; 2001US-0261694P.
PR 12-JAN-2001; 2001US-0261695P.
PR 12-JAN-2001; 2001US-0261697P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Setdel-Dugan C, Ferguson KC, Kidd T;
XX
DR WPI; 2002-559664/64.
DR P-PSDB; AAO18492.
XX
XX
PT Identifying an insulin receptor signaling modulator, useful as drug
PT targets for treating diabetes or metabolic disorders, comprises
PT contacting an assay system comprising insulin receptor signaling
PT modifiers with a test agent.
XX
XX
PS Disclosure; Page 39-41; 232pp; English.
XX
XX
CC The present invention relates to a method of identifying a candidate
CC insulin receptor (INR) signaling modulating agent, involving contacting
CC an assay system comprising an insulin receptor signaling modifier (ISM)
CC polypeptide or nucleic acid with a test agent, and detecting a test agent
CC biased activity of the assay system. The method is useful for
CC identifying candidate INR signaling modulating agents. ISM genes may be
CC used as drug targets for treatment of disorders related to INR signaling
CC such as diabetes or metabolic syndrome. ISM nucleic acids and
CC polypeptides are useful for identifying and testing agents that modulate
CC ISM function and for other applications related to the involvement of ISM
CC in INR signaling, and for identifying subjects having a predisposition to
CC such diseases associated with INR signaling. The present sequence is an
CC ISM coding sequence described in the exemplification of the invention
XX
SQ Sequence 2372 BP; 714 A; 548 C; 519 G; 591 T; 0 U; 0 Other;
XX
Query Match 10.1%; Score 80.4; DB 6; Length 2372;
Best Local Similarity 98.8%; Pred. No. 2.3e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 630 CTGAAGAGAGAGCGTCTCTTCTACACACATTTTACCTTTCTTCTGAATTCATTA 689
DB 1475 CTGAAGAGAGAGCGTCTCTTCTTACTACACCATTTTACCTTTCTTCTGAATTCATTA 1416
CTTCTCTGTAGATTAAGTTCTGT 711
QY 690
DB 1415 CTTCTCTGTAGATTAAGTTCTTT 1394
CTTCTCTGTAGATTAAGTTCTTT 1394
XX
RESULT 26
ACA56791/c
XX ACA56791 standard; cDNA; 2372 BP.
XX
AC ACA56791;
XX
DT 06-JUN-2003 (first entry)
XX
DE Human signaling pathway polynucleotide probe SEQ ID NO 1389.
XX
KW Human; probe; ss; array element; Parkinson's disease;
XX signaling pathway population; cancer; adenocarcinoma; leukaemia;
XX immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX
OS Homo sapiens.
XX
PN US6500938-B1.
XX
PD 31-DEC-2002.
XX
PF 30-JAN-1998; 98US-00016434.

KW p54bAPK MAP kinase; c-Jun kinase 3; JNK3 alpha protein kinase;
KM c-Jun N-terminal kinase 3; stress activated protein kinase beta;
KW chromosome 4q22.1-q23.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH CDS 224..1492
FT /*tag= a
FT /product= "Human MAP kinase MAPK10 (JNK3) protein"
XX
XX MO2004047623-A2.
XX
XX 10-JUN-2004.
XX
XX 25-NOV-2003; 2003MO-US037948.
XX
XX 25-NOV-2002; 2002US-0429136P.
XX
XX 24-JUL-2003; 2003US-0490234P.
XX
XX (SEQU-) SEQUENOM INC.
XX
XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
PI
XX WPI; 2004-441051/41.
XX
XX P-PSDB; ADP45606.
XX
XX Identifying a subject at risk of breast cancer by detecting the presence
PT of polymorphic variations in the ICAM, MAPK10, KIA0861, NIMA1 or GALE
PT regions which are associated with breast cancer in a nucleic acid sample
PT from a subject.
XX
XX
XX Claim 63; SEQ ID NO 9; 289pp; English.
XX
XX The invention relates to a novel method for identifying a subject at risk
CC of breast cancer comprising detecting the presence or absence of one or
CC more polymorphic variations associated with breast cancer in a nucleic
CC acid sample from a subject. The method of the invention has cytostatic
CC applications and may be useful for identifying a subject at risk of
CC breast cancer, for early diagnosis, prevention and treatment of breast
CC cancer, possibly via gene therapy, as well as to analyse and predict a
CC response to a breast cancer treatment and in clinical drug trials. The
CC current sequence is that of the human MAP kinase MAPK10 (JNK3; JNK3A;
CC p493F12;p54bAPK MAP kinase;c-Jun kinase 3;JNK3 alpha protein kinase;c-
CC Jun N-terminal kinase 3;stress activated protein kinase beta) cDNA of the
CC invention which has been mapped to chromosomal position 4q22.1-q23.
XX
XX
XX Sequence 2372 BP; 714 A; 547 C; 521 G; 590 T; 0 U; 0 Other;
SQ
XX
XX Query Match 10.1%; Score 80.4; DB 12; Length 2372;
XX Best Local Similarity 98.8%; Pred. No. 2.3e-08;
XX Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 630 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTGAATTCATTA 689
XX |||||
XX DB 1475 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTGAATTCATTA 1416
XX |||||
XX QY 690 CTTCTTGTAGATAGTTCTGT 711
XX |||||
XX DB 1415 CTTCTTGTAGATAGTTCTTT 1394
XX |||||
XX
XX RESULT 29
XX ADX92938/c
XX ID ADX92938 standard; cDNA; 2372 BP.
XX
XX AC ADX92938;
XX
XX 02-DEC-2004 (first entry)
XX
XX Mitogen-activated protein kinase 10 cDNA.
XX
XX cytosolic; gene therapy; human;
KW

KW branching morphogenesis modulating agent; MEM agent; gene; ss.
XX
XX Homo sapiens.
OS
XX MO2004037990-A2.
XX
XX
XX PN
XX
XX 06-MAY-2004.
XX
XX
XX PD
XX
XX 22-OCT-2003; 2003MO-US033549.
XX
XX
XX 23-OCT-2002; 2002US-0420554P.
XX
XX 30-DEC-2002; 2002US-0436941P.
XX
XX
XX (EXEL-) EXELIXIS INC.
XX
XX Plowman GD, Karim PD, Swimmer C, Habeck HA, Koblizak TI;
PI Schulte-Merker S, Langheinrich U, Scott GM, Trowe T, Vogel AM;
PI Odenhal JH, Scheel JK, Will TT, Jin Y, Bjerke LM, Hal B;
PI Adamkiewicz JI, Lickelg K, Hammonds RGR, Amundsen CD, Zhang H;
PI Nicoll M;
XX
XX WPI; 2004-365506/34.
XX
XX P-PSDB; ADX92969.
XX
XX
XX Identifying a candidate branching morphogenesis modulating agent for
PT treating cancer comprises contacting the assay system comprising a MEM
PT polypeptide or nucleic acid with a test agent and detecting a test agent-
PT biased activity.
XX
XX Example 3; SEQ ID NO 9; 179pp; English.
XX
XX The invention describes a method of identifying a candidate branching
CC morphogenesis modulating (MEM) agent. The method comprises: providing an
CC assay system comprising a MEM polypeptide or nucleic acid; contacting the
CC assay system with a test agent under conditions where the system provides
CC a reference activity, except for the presence of the test agent; and
CC detecting a test agent-biased activity of the assay system, where a
CC difference between the test agent-biased activity and the reference
CC activity identifies the test agent as a candidate branching morphogenesis
CC modulating agent. Also described are: a method of modulating branching
CC morphogenesis in a mammalian cell; and a method for diagnosing a disease
CC in a patient. The method is useful in identifying a candidate branching
CC morphogenesis modulating agent for preparing a composition for diagnosing
CC or treating cancer. This sequence encodes a human branching morphogenesis
CC modulating (MEM) protein.
XX
XX
XX Sequence 2372 BP; 714 A; 547 C; 521 G; 590 T; 0 U; 0 Other;
SQ
XX
XX Query Match 10.1%; Score 80.4; DB 13; Length 2372;
XX Best Local Similarity 98.8%; Pred. No. 2.3e-08;
XX Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 630 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTGAATTCATTA 689
XX |||||
XX DB 1475 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTGAATTCATTA 1416
XX |||||
XX QY 690 CTTCTTGTAGATAGTTCTGT 711
XX |||||
XX DB 1415 CTTCTTGTAGATAGTTCTTT 1394
XX |||||
XX
XX RESULT 30
XX ADX98578/c
XX ID ADX98578 standard; cDNA; 2372 BP.
XX
XX AC ADX98578;
XX
XX 05-MAY-2005 (first entry)
XX
XX Human mitogen-activated protein kinase 10 (MAPK10) cDNA.
XX
XX SNP detection; breast tumor; endocrine disease;
XX
XX gynecology and obstetrics; neoplasm; cytostatic; metastasis;
KW

KM Gene therapy; RNA interference; chromosome 4; ss; gene;
KM Mitogen-activated protein kinase 10; Jun N terminal kinase-3; MAPK10.
XX Homo sapiens.
XX MO2005014846-A2.
XX
XX 17-FEB-2005.
PD
XX 27-MAY-2004; 2004MO-US016939.
PF
XX 24-JUL-2003; 2003JUS-0490234P.
PR 25-NOV-2003; 2003JUS-00723681.
PR 25-NOV-2003; 2003JUS-0525239P.
XX
XX (SEQU-) SEQUENOM INC.
XX
XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
PI Hoyal-Wrightson CR;
PI WPI; 2005-163257/17.
DR P-PSDB; ADX98588.
XX
XX Identifying risk of, preventing and/or treating breast cancer by
PT identifying and/or analyzing polymorphic variations in nucleotide
PT sequences within the human genome.
XX
XX Claim 22; SEQ ID NO 11; 617bp; English.
XX
XX The invention relates to a novel method for identifying a subject at risk
CC of breast cancer comprising detecting the presence or absence of a
CC polymorphic variation associated with breast cancer. The method of the
CC invention demonstrates cytostatic activity and may be useful for
CC identifying a risk of, preventing and/or treating breast cancer and
CC cancer metastasis. The methods may be utilized for gene therapy or RNA
CC interference. The current sequence is that of the human mitogen-activated
CC protein kinase 10 (MAPK10) cDNA of the invention which is located at
CC chromosome 4q22.1-q23.
XX
XX Sequence 2372 BP; 714 A; 547 C; 521 G; 590 T; 0 U; 0 Other;
SQ
XX
XX Query Match 10.1%; Score 80.4; DB 14; Length 2372;
Best Local Similarity 98.8%; Pred. No. 2.3e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTCTTTCTTGAATTCATTA 689
DB 1475 CTGAAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTCTTTCTTGAATTCATTA 1416
QY 690 CTTCCTTGATGATGATTCGT 711
DB 1415 CTTCCTTGATGATGATTCGT 1394
RESULT 31
AEG09273/c
XX AEG09273 standard; DNA; 2372 BP.
XX
XX AEG09273;
AC
XX
XX 20-APR-2006 (first entry)
DT
XX
XX Human MAPK10, transcript variant 1 DNA.
DE
XX
XX amyloid-beta precursor protein; pharmaceutical;
KM amyloid-beta precursor protein; pharmaceutical;
KM Alzheimer's disease; degeneration; cognitive disorder; Neuroprotective;
KM Nootropic; substrate; mitogen-activated protein kinase 10; MAPK10; ds;
XX gene.
XX Homo sapiens.
XX
XX Key Location/Qualifiers

FT CDS 224..1492
FT /tag= a
FT /product= "mitogen-activated protein kinase 10 (MAPK10),
FT transcript variant 1"
XX
XX
XX MO2005109001-A2.
XX
XX 17-NOV-2005.
PD
XX
XX 12-MAY-2005; 2005MO-EP052182.
PF
XX 12-MAY-2004; 2004US-0570352P.
PR 24-APR-2004; 2004US-0603948P.
XX
XX (GALA-) GALAPAGOS GENOMICS NV.
PA (LAEN/) LAENEN W.
XX
XX Splitteels KF, Hoffmann M, Merchiers PG;
PI
XX WPI; 2006-231019/24.
DR P-PSDB; AEG09282.
DR REFSEQ; NM_002753.
XX
XX Identifying a compound that inhibits amyloid-beta precursor protein
PT processing in a mammalian cell for treating e.g., Alzheimer's disease by
PT measuring a compound-polypeptide property related to amyloid-beta peptide
PT production.
XX
XX Example 1; SEQ ID NO 9; 84bp; English.
XX
XX This invention describes a novel method of identifying a compound that
CC inhibits the processing of amyloid-beta precursor protein in a mammalian
CC cell. The invention also describes: a) an agent for inhibiting amyloid-
CC beta precursor processing consisting of an antisense polynucleotide, a
CC ribozyme or a small interfering RNA (siRNA), where the agent comprises a
CC nucleic acid sequence complementary to, or engineered from, a naturally-
CC occurring polynucleotide sequence encoding the polypeptide comprising the
CC amino acid sequence of AEG09278 or AEG09279 and b) a pharmaceutical
CC composition comprising the agent for inhibiting amyloid-beta precursor
CC processing or an amyloid-beta precursor processing-inhibiting amount of a
CC mitogen activated protein-kinase inhibitor in admixture with a carrier.
CC The method involves activation of a biological pathway producing an
CC indicator of the processing of amyloid-beta precursor protein e.g. a
CC phosphorylated substrate of a kinase comprising AEG09266-AEG09268. The
CC indicator induces the expression of a reporter e.g. alkaline phosphatase,
CC GFP, dGFP, luciferase or beta-galactosidase in the mammalian cell.
CC The pharmaceutical composition further comprises a label indicating use
CC of the composition for treating or preventing a condition involving
CC cognitive impairment or a susceptibility to the condition. The agent is
CC useful in the manufacture of a medicament for inhibiting the processing
CC of amyloid-beta precursor protein in a subject suffering from or
CC susceptible to the abnormal processing of the protein, or for treating or
CC preventing a condition involving cognitive impairment or a susceptibility
CC to the condition, preferably, Alzheimer's disease. This sequence encodes
CC human mitogen-activated protein kinase 10 (MAPK10), transcript variant 1,
CC a kinase involved in the up-regulation of amyloid-beta 1-42.
XX
XX Sequence 2372 BP; 714 A; 547 C; 521 G; 590 T; 0 U; 0 Other;
SQ
XX
XX Query Match 10.1%; Score 80.4; DB 15; Length 2372;
Best Local Similarity 98.8%; Pred. No. 2.3e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTCTTTCTTGAATTCATTA 689
DB 1475 CTGAAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTCTTTCTTGAATTCATTA 1416
QY 690 CTTCCTTGATGATGATTCGT 711
DB 1415 CTTCCTTGATGATGATTCGT 1394
RESULT 32

ACC46216/c
ID ACC46216 standard; cDNA, 2945 BP.
XX
AC ACC46216;
XX
02-JUN-2003 (first entry)
DT
XX Human dithp intracellular signalling protein-encoding cDNA.
DE
XX Human; dithp, diagnostic and therapeutic polynucleotide; diagnosis;
XX cancer; cell proliferative disorder; autoimmune disorder;
XX inflammatory disorder; infection; hormonal disorder; metabolic disorder;
XX neurological disorder; gastrointestinal disorder; transport disorder;
XX connective tissue disorder; drug screening; proteome analysis;
XX gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
XX disease model; toxicological testing; transcript imaging;
XX intracellular signalling; gene; ss.
XX
XX Homo sapiens.
XX
XX MO200297031-A2.
XX
XX 05-DEC-2002.
XX
XX 27-MAR-2002; 2002WO-US010056.
XX
XX 28-MAR-2001; 2001US-0279619P.
XX 29-MAR-2001; 2001US-028067P.
XX 29-MAR-2001; 2001US-028068P.
XX 16-MAY-2001; 2001US-0291280P.
XX 17-MAY-2001; 2001US-0291829P.
XX 17-MAY-2001; 2001US-0291849P.
XX 19-JUN-2001; 2001US-0299428P.
XX 20-JUN-2001; 2001US-0299776P.
XX 20-JUN-2001; 2001US-0300001P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J,
XX Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amehy SR,
XX Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstein EH,
XX Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B,
XX Flores V, Marwaha R, Lo A, Lan RV, Urashka ME,
XX
XX WPI; 2003-129518/12.
XX P-PSDB; ABR41274.
XX
XX Novel human diagnostic and therapeutic polypeptide useful for identifying
XX test compound which specifically binds to a polypeptide encoded by human
XX diagnostic and therapeutic polynucleotide, and to induce antibodies.
XX
XX Claim 2; SEQ ID NO 137; 591pp; English.
XX
XX The invention relates to novel human diagnostic and therapeutic
XX polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded
XX proteins (DITHP; ABR41136-ABR41812). The invention also relates to
XX polynucleotide sequences at least 90% identical to the dithp cDNA
XX sequences of the invention; recombinant vectors, host cells and
XX transgenic organisms comprising a dithp nucleic acid sequence; the
XX recombinant production of DITHP proteins; antibodies specific for DITHP
XX proteins; microarrays comprising dithp nucleic acid sequences; methods of
XX detecting dithp nucleotide and protein sequences; methods of screening
XX for compounds which specifically bind a DITHP protein; and methods of
XX assessing the toxicity of test compounds using a dithp hybridisation
XX probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
XX diagnosis of a wide variety of conditions including cancer and other cell
XX proliferative disorders; autoimmune or inflammatory disorders; bacterial,
XX viral, fungal or parasitic infections; hormonal disorders; metabolic
XX disorders; neurological disorders; gastrointestinal disorders; transport
XX disorders; and connective tissue disorders. They may also be used to
XX screen for modulators of protein activity or gene expression. DITHP
XX proteins can additionally be used in analysis of the proteome of a tissue
XX or cell type and to induce antibodies. The dithp nucleic acids are

CC additionally useful in somatic or germline gene therapy of the disorders
CC mentioned above, as a source of antisense sequences, as a source of
CC probes and primers, in genotyping and identification of individuals, in
CC the generation of transgenic animal models of human disease or knock in
CC humanised animals, in toxicological testing, and in transcript imaging.
CC The present sequence represents a dithp cDNA encoding a DITHP protein
CC which has intracellular signalling activity. Note: the sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 2945 BP; 878 A; 637 C; 671 G; 759 T; 0 U; 0 Other;
XX
XX Query Match 10.1%; Score 80.4; DB 8; Length 2945;
XX Best Local Similarity 98.8%; Pred. No. 2.4e-08;
XX Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 630 CTGAGGAGAGAGGCTGCTTACTACACCATTTTACGCTTCTTCTGAAATTCATTA 689
XX |||||||
XX Db 1533 CTGAGGAGAGAGGCTGCTTACTACACCATTTTACGCTTCTTCTGAAATTCATTA 1474
XX |||||||
XX QY 690 CTTCCTGTAGATATGATCTGT 711
XX |||||||
XX Db 1473 CTTCCTGTAGATATGATCTTT 1452
XX |||||||
XX
XX RESULT 33
XX ADI61665/c
XX ID ADI61665 standard; cDNA; 2982 BP.
XX
XX AC ADI61665;
XX
XX DT 22-APR-2004 (first entry)
XX
XX DE Human cDNA downregulated in Alzheimer's disease, INCYTE 413797.7.
XX
XX KW Human; ss; Alzheimer's disease; differential display; neuroprotective;
XX brain disorder.
XX
XX OS Homo sapiens.
XX
XX PN US6682888-B1.
XX
XX PD 27-JUN-2004.
XX
XX XX 05-MAY-2000; 2000US-00566921.
XX PF
XX PR 05-MAY-2000; 2000US-00566921.
XX
XX PA (INCY-) INCYTE CORP.
XX
XX PI Loring JF, Tingley DW, Edwards CW,
XX
XX WPI; 2004-118572/12.
XX
XX PT New composition comprising cDNAs that are differentially expressed in
XX brain disorders, useful for diagnosing or treating Alzheimer's disease.
XX
XX PS Claim 1; SEQ ID NO 33; 223pp; English.
XX
XX The invention relates to a new composition comprising ADI61633-
XX ADI61770 and their complements that are cDNAs differentially expressed in
XX brain disorders. Also included are a high throughput method for detecting
XX differential expression of one or more cDNAs in a sample containing
XX nucleic acids and a high throughput method for screening a library of
XX molecules or compounds to identify a ligand that specifically binds a
XX cDNA. The expression of the each of the cDNAs is downregulated at least
XX two-fold in the brain of the subjects with Alzheimer's disease (ADI61633-
XX ADI61770) or upregulated at least two fold in Alzheimer's disease
XX (ADI61728-ADI61770). The composition is useful for diagnosing or treating
XX Alzheimer's disease. The present sequence is a cDNA downregulated at
XX least two-fold in the brain of the subjects with Alzheimer's disease.

Sequence 2982 BP; 868 A; 617 C; 669 G; 781 T; 0 U; 47 Other;
Query Match 10.1%; Score 80.4; DB 12; Length 2982;
Best Local Similarity 98.8%; Pred. No. 2.4e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 630 CTGAAGAGAGAGGCTGCTCTTACTACACATTTTACTCTTCTTCTGAATTCATTA 689
DB 1570 CTGAAGAGAGAGGCTGCTCTTACTACACATTTTACTCTTCTTCTGAATTCATTA 1511
QY 690 CTTCCTGTAGATTAAGTTCTGT 711
DB 1510 CTTCCTGTAGATTAAGTTCTTT 1489

RESULT 34
AEA43830/c
ID AEA43830 standard; cDNA; 2982 BP.
XX
XX AEA43830;
AC
XX 25-AUG-2005 (first entry)
DT
XX
XX Human cDNA differentially expressed in brain tissue SEQ ID NO:33.
DE
XX
XX diagnosis; treatment; brain disease; neuroprotective; cerebroprotective;
KM muscular-gen.; cytotoxic; neuroleptic; nootropic; antidepressant;
KW anticonvulsant; analgesic; antiparkinsonian; ophthalmological;
XX immunotherapy; gene therapy; ss.
XX
XX Homo sapiens.
OS
XX
XX US2005130171-A1.
PN
XX
XX 16-JUN-2005.
PD
XX
XX 26-JAN-2004; 2004US-00765700.
PF
XX
XX 05-MAY-2000; 2000US-00566921.
PR
XX
XX (INCY-) INCYTE CORP.
PA
XX
XX Loring JF, Tingley DW, Edwards CM;
PI
XX
XX WPI; 2005-456990/46.
DR
XX
XX
XX Composition useful for diagnosis, staging, treating or monitoring
PT treatment of a subject with a brain disorder, comprises several cDNAs
PT that are differentially expressed in brain disorders.
XX
XX Claim 1, SEQ ID NO 33; 231pp; English.
PS

The invention relates to a composition (I) for the diagnosis, staging, treatment or for the monitoring of treatment of a subject with a brain disorder. (I) comprises several cDNAs that are differentially expressed in brain disorders and chosen from any one of 138 nucleotide sequences of AEA43798-AEA43935, or their complements. Also described: (1) a high throughput method for detecting differential expression of one or more cDNAs in a sample containing nucleic acids; (2) an isolated cDNA (II) selected from AEA43812, AEA43813, AEA43830, AEA43831, AEA43855, AEA43856, AEA43883 and AEA43923; (3) an expression vector (III) containing (II); (4) a host cell (IV) containing (III); (5) a protein (V) produced using (IV); and (6) a pharmaceutical composition comprising (V). (I) is useful for a high throughput method of screening a library of molecules or compounds to identify a ligand which specifically binds a cDNA, where the method involves combining (I) with the library of molecules or compound under conditions to allow specific binding and detecting specific binding between each cDNA and a molecule or compound. (IV) is useful for producing a protein, which involves culturing (IV) under conditions for the expression of the protein and recovering the protein from the culture. (V) is useful for high throughput method for screening a library of molecules or compounds to identify a ligand which specifically binds (V), where the method involves combining (V) or its portion with the

library of molecules or compound under conditions to allow specific binding and detecting specific binding between (V) and a molecule or compound. (V) is useful for purifying a ligand from a sample, which involves combining (V) or its portion with the sample under conditions to allow specific binding, recovering the bound protein and separating the protein from ligand. (V) is also useful for producing an antibody, which involves immunizing an animal with (V) or its portion under conditions to elicit an antibody response, isolating animal antibodies and screening the isolated antibodies with the protein. (II) is useful in gene therapy for the treatment or prevention of conditions and disorders associated with immune response. The present sequence represents a human cDNA sequence which is differentially expressed in brain tissues, which is used in the exemplification of the present invention.

Sequence 2982 BP; 868 A; 617 C; 669 G; 781 T; 0 U; 47 Other;
Query Match 10.1%; Score 80.4; DB 14; Length 2982;
Best Local Similarity 98.8%; Pred. No. 2.4e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 630 CTGAAGAGAGAGGCTGCTCTTACTACACATTTTACTCTTCTTCTGAATTCATTA 689
DB 1570 CTGAAGAGAGAGGCTGCTCTTACTACACATTTTACTCTTCTTCTGAATTCATTA 1511
QY 690 CTTCCTGTAGATTAAGTTCTGT 711
DB 1510 CTTCCTGTAGATTAAGTTCTTT 1489

RESULT 35
AAH47044/c
ID AAH47044 standard; DNA; 8749 BP.
XX
XX AAH47044;
AC
XX
XX 29-OCT-2001 (first entry)
DT
XX
XX Nucleotide sequence of pFastFind-jnk3 vector.
DE
XX
XX IRES; internal ribosome initiation sequence; promoter; surface marker;
KM label protein; membrane protein; ds.
XX
XX
XX Synthetic.
OS
XX
XX WO200157212-A1.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 02-FEB-2001; 2001WO-US003411.
PF
XX
XX 02-FEB-2000; 2000US-0179893P.
PR
XX
XX (ICON-) ICONIX PHARM INC.
PA
XX
XX Jarnigan K, Zhou H;
PI
XX
XX WPI; 2001-476284/51.
DR
XX
XX Polynucleotide for rapid isolation of candidate eukaryotic cell clones
PT comprises a promoter, a test gene, an IRES sequence and a surface marker.
PT
XX
XX Example; Page 32-37; 32pp; English.
PS

The invention relates to a polynucleotide (I) comprising: (a) a regulatable promoter; (b) a test gene; (c) an IRES sequence; and (d) a surface marker coding sequence comprising a secretion signal sequence, a detectable label protein and a membrane protein where expression of the test gene also results in expression of the surface marker. A method is provided for identifying a host cell that exhibits regulated expression of a test gene complex that comprises (a) providing more than one host cell; (b) inducing the promoter; and (c) selecting a host cell that displays the surface marker on its surface. (I), the host cell and the method are useful for the rapid isolation of candidate eukaryotic cell

CC clones in which a query gene is regulated by exogenous application of an
CC appropriate stimulus. The present sequence represents the nucleotide
CC sequence of a pFastbind-Jmk3 vector

SO Sequence 8749 BP; 2128 A; 2329 C; 2287 G; 2005 T; 0 U; 0 Other;

Query Match 10.1%; Score 80.4; DB 4; Length 8749;

Best Local Similarity 98.8%; Pred. No. 3e-08; Mismatches 1; Indels 0; Gaps 0;

Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 630 CTGAAGGAGGAGGCTGCTCTTCTTACTACACCATTTTGTCTTTCTTCTGAATTCATTA 689

DB 1781 CTGAAGGAGGAGGCTGCTCTTCTTACTACACCATTTTGTCTTTCTTCTGAATTCATTA 1722

DB 690 CTTCCTGTAGATAGTCTGT 711

DB 1721 CTTCCTGTAGATAGTCTGT 1700

RESULT 36

AAT10640/C

ID AAT10640 standard; CDNA; 1975 BP.

AC AAT10640;

AT 26-APR-1996 (first entry)

DE Stress activated protein kinase p54 beta-I cDNA.

KM Stress activated protein kinase; SAPK; p54 beta-I; antibody;

KM inflammation; hypoxia; heat stress; ss.

OS Rattus sp.

XX Key Location/Qualifiers

FT CDS 364..1644

FT /*tag= a

PN CA2148898-A.

PD 10-NOV-1995.

PF 08-MAY-1995; 95CA-02148898.

PR 09-MAY-1994; 94US-00240014.

PA (GEHO) GEN HOSPITAL CORP.

PA (ONTA-) ONTARIO CANCER INST.

PI Kyriakis JM, Avruch J, Banerjee P, Woodgett JR;

DR WPI; 1996-106355/12.

XX DNA encoding recombinant p54 stress activated protein kinase - and

PT related antibodies, useful for treating inflammation, hypoxia and heat

PT stress, and for drug screening.

PS Claim 20; Page 44-45; 68pp; English.

XX A cDNA clone (AAT10640) was obtd. that codes for rat proline-directed

CC stress-activated protein kinase (SAPK) p54 beta-I (AAR89410). This cDNA,

CC and others (see AAT10638-39 and AAT10641-42) coding for p54 alpha-I,

CC alpha-II, beta-I and gamma (AAR89408-9 and AAR89411-12), were isolated

CC from a rat brain cDNA library following PCR amplification using primers

CC based on p54 tryptic peptides obt. from a cycloheximide-treated rat

XX

DB 1505 GCACCTGAAGTGAAGGCTGCTCTTCTTACTACACCATTTTGTCTTTCTTCTGAATTC 1446

DB 686 ATTACTCTCTGTAGATAGTCTGT 711

DB 1445 ATTACTCTCTGTAGATAGTCTGT 1420

RESULT 37

ABL88414/C

ID ABL88414 standard; CDNA; 1975 BP.

AC ABL88414;

AT 16-MAY-2002 (first entry)

DE Pain regulated CDNA sequence 57.

KM Pain; analgesic; gene therapy; neurological disorder;

KM neurodegenerative disease; gene; ss.

OS Rattus sp.

XX WO200212338-A2.

PD 14-FEB-2002.

PF 03-AUG-2001; 2001WO-EP009011.

PR 03-AUG-2000; 2000DE-01037759.

PA (CHEF) GRUNENTHAL GMBH.

PI Gullen C, Wetzel S, Weihe E, Schaefer MK;

DR WPI; 2002-257469/30.

PT P-PSDB; ABB85009.

PT Identifying pain-regulating compounds, useful for treating chronic pain

PT and for diagnosis, by measuring binding of compounds to specific peptides

PS Claim 1; Fig 34; 213pp; German.

XX The invention relates to identifying pain-regulating substances (A)

CC comprises (i) incubating a test substance with a cell (or preparation

CC from it) that has synthesised a peptide or protein (B) and (ii) measuring

CC either binding of the test substance to (B) or some functional parameter

CC that is altered by this binding. The method is useful for identifying

CC pain-regulating substances (A) with analgesic activity. (A) along with

CC nucleic acid (ABL88411-ABL88441) that encode proteins (B, ABB85006-

CC ABB85037) that interact with (A); (B); vectors containing the nucleic

CC acid; antibodies against (B); cells that express (B) and agents that bind

CC to (B); are all useful for treating pain, particularly chronic pain,

CC including use in gene therapy. The same materials can also be used for

CC diagnosis, e.g. of neurological and neurodegenerative diseases. The

CC present sequence is that of a polynucleotide of the invention

XX

SO Sequence 1975 BP; 556 A; 506 C; 488 G; 425 T; 0 U; 0 Other;

Query Match 8.3%; Score 66.8; DB 6; Length 1975;

Best Local Similarity 86.0%; Pred. No. 2.8e-05; Mismatches 12; Indels 0; Gaps 0;

Matches 74; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

DB 686 ATTACTCTCTGTAGATAGTCTGT 711

DB 1505 GCACCTGAAGTGAAGGCTGCTCTTCTTACTACACCATTTTGTCTTTCTTCTGAATTC 685

DB 1445 ATTACTCTCTGTAGATAGTCTGT 1420

QY 626 GTACCTGAAGGAGGCTGCTCTTCTTACTACACCATTTTGTCTTTCTTCTGAATTC 685

QY 626 GTACCTGAAGGAGGCTGCTCTTCTTACTACACCATTTTGTCTTTCTTCTGAATTC 685

```

RESULT 38
ABU8413/c
ID ABU8413 standard; cDNA; 1240 BP.
XX
XX
AC ABU8413;
XX
XX
DT 16-MAY-2002 (first entry)
XX
DE Pain regulated cDNA sequence 56.
XX
XX
KM Pain; analgesic; gene therapy; neurological disorder;
KM neurodegenerative disease; gene; ss.
XX
XX
OS Mus sp.
XX
XX
PN WO200212338-A2.
XX
PD 14-FEB-2002.
XX
PF 03-AUG-2001; 2001MO-EP009011.
XX
PR 03-AUG-2000; 2000DE-01037759.
XX
XX
PA (CHEF) GRUENENTHAL GMBH.
XX
PI Gyllen C, Metzels I, Wrendt S, Weihe E, Schaefer MK;
XX
DR WPI; 2002-257469/30.
DR P-PSDB; AB85008.
XX
XX
PT Identifying pain-regulating compounds, useful for treating chronic pain
PT and for diagnosis, by measuring binding of compounds to specific peptides
PT and proteins.
XX
XX
PS Claim 1; Fig 34; 213pp; German.
XX
XX
CC The invention relates to identifying pain-regulating substances (A);
CC comprises (i) incubating a test substance with a cell (or preparation
CC from it) that has synthesised a peptide or protein (B) and (ii) measuring
CC either binding of the test substance to (B) or some functional parameter
CC that is altered by this binding. The method is useful for identifying
CC pain-regulating substances (A) with analgesic activity. (A) along with
CC nucleic acid (ABU8411-ABU8441) that encode proteins (B, AB85006-
CC AB85037) that interact with (A); (B); vectors containing the nucleic
CC acid; antibodies against (B); cells that express (B) and agents that bind
CC to (B), are all useful for treating pain, particularly chronic pain;
CC including use in gene therapy. The same materials can also be used for
CC diagnosis, e.g. of neurological and neurodegenerative diseases. The
CC present sequence is that of a polynucleotide of the invention
XX
XX
SQ Sequence 1240 BP; 359 A; 299 C; 317 G; 265 T; 0 U; 0 Other;
Query Match 8.2%; Score 66; DB 6; Length 1240;
Best Local Similarity 87.8%; Pred. No. 3.8e-05;
Matches 72; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 630 CTGAAGAGAGAGGCTGCTCTTACTACACATTTTACTCTTCTTCTGAAATCATTA 689
DB 1201 CTGAAGCGGAGGGCTGCTTGTACACGCAATTCCTTCTTCTGAGTTCAATTA 1442
QY 690 CTTCCTTGTAGATAGTTCTGT 711
DB 1141 CTTCCTTGTAGATAGTTCTTT 1120

```

```

DE Stress activated protein kinase p54 beta-II cDNA.
XX
XX
KM Stress activated protein kinase; SAPK; p54 beta-II; antibody;
KM inflammation; hypoxia; heat stress; ss.
XX
XX
OS Rattus sp.
XX
XX
FH Key Location/Qualifiers
FT CDS 364..1644
FT FT /*tag= a
FT misc_difference 1549
FT FT /*tag= b
FT FT /*note= "base 1549 is unclear in the specification,
FT FT probably C or G"
FT misc_difference 1550
FT FT /*tag= C
FT FT /*note= "base 1550 is unclear in the specification,
FT FT probably C or G"
XX
XX
PN CA2148898-A.
XX
XX
PD 10-NOV-1995.
XX
XX
PF 08-MAY-1995; 95CA-02148898.
XX
XX
PR 09-MAY-1994; 94US-00240014.
XX
XX
PA (GENO) GEN HOSPITAL CORP.
XX
XX
PA (ONTA-) ONTARIO CANCER INST.
XX
XX
PI Kyriakis JM, Avruch J, Banerjee P, Woodgett JR;
XX
DR WPI; 1996-106355/12.
DR P-PSDB; AAR89411.
XX
XX
PT DNA encoding recombinant p54 stress activated protein kinase - and
PT related antibodies, useful for treating inflammation, hypoxia and heat
PT stress, and for drug screening.
XX
XX
PS Claim 21; Page 46-47; 68pp; English.
XX
XX
CC A cDNA clone (AAT10641) was obt'd. that codes for rat proline-directed
CC stress-activated protein kinase (SAPK) p54 beta-II (AAR89411). This cDNA,
CC and others (see AAT10638-40 and AAT10642) coding for p54 alpha-I, alpha-
CC II, beta-I and gamma (AAR89408-10 and AAR89412), were isolated from a rat
CC brain cDNA library following PCR amplification using primers based on p54
CC tryptic peptides obt. from a cycloheximide-treated rat
XX
XX
SQ Sequence 1986 BP; 559 A; 510 C; 488 G; 427 T; 0 U; 2 Other;
Query Match 8.1%; Score 64.4; DB 2; Length 1986;
Best Local Similarity 86.6%; Pred. No. 9.7e-05;
Matches 71; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 630 CTGAAGAGAGAGGCTGCTCTTACTACACATTTTACTCTTCTTCTTCTGAAATCATTA 689
DB 1507 CTGAAGTAGAGGCTGCGCTTGTACCTACGCGCTTCTTCTTCTTCTGAGTTCAATTA 1448
QY 690 CTTCCTTGTAGATAGTTCTGT 711
DB 1447 CTTCCTTGTAGATAGTTCTTT 1426

```

```

RESULT 39
AAT10641/c
ID AAT10641 standard; cDNA; 1986 BP.
XX
XX
AC AAT10641;
XX
XX
DT 26-APR-1996 (first entry)
XX
XX

```

```

RESULT 40
AAT10642/c
ID AAT10642 standard; cDNA; 1408 BP.
XX
XX
AC AAT10642;
XX
XX
DT 26-APR-1996 (first entry)
XX
XX
DE Stress activated protein kinase p54 gamma cDNA.
XX
XX

```


KW Stress activated protein kinase; SAPK; p54 gamma; antibody; inflammation;
KM hypoxia; heat stress; ss.
XX
XX Rattus sp.
OS
XX Key Location/Qualifiers
FH CDS 176..1408
FT /*tag= a
XX
XX CA2148898-A.
XX
XX 10-NOV-1995.
XX
XX 08-MAY-1995; 95CA-02148898.
XX
XX 09-MAY-1994; 94US-00240014.
XX
XX (GENO) GEN HOSPITAL CORP.
XX (ONTA-) ONTARIO CANCER INST.
XX
XX Kyriakis JM, Avruch J, Banerjee P, Woodgett JR;
XX WPI; 1996-106355/12.
XX P-PSDB; AAR89412.
XX
XX DNA encoding recombinant p54 stress activated protein kinase - and
XX related antibodies, useful for treating inflammation, hypoxia and heat
XX stress, and for drug screening.
XX
XX Claim 22; Page 47-48; 68pp; English.
XX
XX A cDNA clone (AA110642) was obtd. that codes for rat proline-directed
XX stress-activated protein kinase (SAPK) p54 gamma (AAR89412). This cDNA,
XX and others (see AA110658-41) coding for p54 alpha-I, alpha-II, beta-I and
XX beta-II (AAR89408-11), were isolated from a rat brain cDNA library
XX following PCR amplification using primers based on p54 tryptic peptides
XX obt. from a cycloheximide-treated rat
XX
XX Sequence 1408 BP; 408 A; 310 C; 339 G; 351 T; 0 U; 0 Other;
SQ

Query Match 6.3%; Score 50.8; DB 2; Length 1408;
Best Local Similarity 74.4%; Pred. No. 0.11;
Matches 64; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGCTGCTTTACTACACCAATTTTACTCTTCTTGAATTC 685
DB 1317 GCACCTAAGAGAGAGCGCTGCTCTTATAGAGCAATCTTAGTCCCTCCAAATCC 1258
QY 686 ATTACTCTCTGTAGATAGTTCTGT 711
DB 1257 ATGACCTCTGTATATCAAGTTCTTT 1232

RESULT 41
ABT09489/c
ID ABT09489 standard; DNA; 580 BP.
XX
XX ABT09489;
AC
XX
XX 05-DEC-2002 (first entry)
DT
XX
XX Phase-1 Rat CT gene SEQ ID No 577.
DE
XX
XX Rat; toxicity study; rat toxic response gene; toxicological response;
KM drug development; phase-1 rat CT gene; ds.
XX
XX Rattus sp.
OS
XX
XX WO200266682-A2.
PN
XX
XX 29-AUG-2002.
PD
XX
XX 29-JAN-2002; 2002WO-US002935.
PF

XX
XX 29-JAN-2001; 2001US-0264933P.
PR
XX 26-JUL-2001; 2001US-0308161P.
PR
XX
XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
PA
XX
XX Farris G, Hicken SH, Farr SB;
PI
XX
XX WPI; 2002-674961/72.
DR
XX
XX
XX Evaluating the toxicity of an agent, useful in drug development or in
XX determining toxicological responses to a new drug, by determining the
XX expression of rat toxicologically relevant genes in the test animal in
XX response to the test agent.
XX
XX
XX Disclosure; Page 247; 388pp; English.
XX
XX The invention relates to a method used for evaluating the toxicity of an
XX agent comprising determining the expression of a rat toxic response
XX gene(s) in the test animal in response to the agent. The method is useful
XX in drug development, particularly for conducting toxicity studies and
XX analysis before a new drug or compound is approved for human consumption
XX or use. The method is also useful in determining toxicological responses
XX to a new drug. This polynucleotide sequence represents a phase-1 rat CT
XX gene of the invention
XX
XX Sequence 580 BP; 170 A; 129 C; 145 G; 125 T; 0 U; 11 Other;
SQ

Query Match 6.2%; Score 49.4; DB 6; Length 580;
Best Local Similarity 74.7%; Pred. No. 0.19;
Matches 62; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 629 CCTGAAGAGAGAGCTGCTTTACTACACCAATTTTACTCTTCTTGAATTCAT 688
DB 494 CCTAAGAGAGAGAGCGCTGCTCTTATAGAGCAATCTTAGTCCCTCCAAATCATG 435
QY 689 ACTTCTCTGTAGATAGTTCTGT 711
DB 434 ACCTCTCTGTATATCAAGTTCTTT 412

RESULT 42
ADG30924/c
ID ADG30924 standard; DNA; 580 BP.
XX
XX ADG30924;
AC
XX
XX 26-FEB-2004 (first entry)
DT
XX
XX Liver toxicity predictive DNA 104.
DE
XX
XX Liver toxicity; Norway rat; 24 hour combo All; ds.
KM
XX
XX Unidentified.
OS
XX
XX WO2003085083-A2.
PN
XX
XX 16-OCT-2003.
PD
XX
XX 01-APR-2003; 2003WO-US010141.
PF
XX
XX 01-APR-2002; 2002US-0369287P.
PR
XX
XX (PHAS-) PHASE 1 MOLECULAR TOXICOLOGY.
PA
XX
XX Kler L, Nolan TD, Sankar U, Derbel M;
PI
XX
XX WPI; 2003-804300/75.
DR
XX
XX Predicting the liver toxicity of an agent to an individual by using the
XX test expression profile with a set of reference expression profiles in a
XX Predictive Model to determine whether the agent will reduce liver
XX toxicity in the individual.
PT

XX Claim 2; Page 168; 379pp; English.
XX
XX The invention relates to a novel method for predicting the liver toxicity
CC of an agent to an individual comprising obtaining a biological sample
CC from an individual treated with the agent, measuring the expression of
CC one or more liver toxicity predictive genes in the sample and using the
CC test expression profile with a set of reference expression profiles in a
CC predictive model to determine whether the agent will reduce liver
CC toxicity in the individual. The method of the invention may be useful for
CC predicting the liver toxicity of an agent to an individual. The current
CC sequence is that of the liver toxicity predictive DNA of the invention
CC which represents a 24 hour combo All gene.
XX
SQ Sequence 580 BP; 170 A; 129 C; 145 G; 125 T; 0 U; 11 Other;
Query Match 6.2%; Score 49.4; DB 10; Length 580;
Best Local Similarity 74.7%; Pred. No. 0.19;
Matches 62; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
OY 629 CCTGAAGAGAGAGCGCTCTCTTACTACACCATTTTACTTTCTTCTGAATTCATT 688
DB 494 CCTAAAGAGAGAGCGCTCTCTTACTACACCATTTTACTTTCTTCTGAATTCATT 435
OY 689 ACTTCTGTAGATAGTTCGT 711
DB 434 ACCTCTGTATATCATGTTCTTT 412
RESULT 43
ADG45512/c
ID ADG45512 standard; DNA; 580 BP.
XX
XX ADG45512;
AC
XX 26-FEB-2004 (first entry)
DT
XX
XX Liver inflammatory predictive gene related DNA sequence.
DE
XX liver; liver toxicity; liver toxicity predictive gene;
XX liver inflammation predictive gene; inflammation; gene; ds; rat.
XX
XX Rattus norvegicus.
OS
XX
XX MO2003095624-A2.
PN
XX 20-NOV-2003.
PD
XX
XX 09-MAY-2003; 2003MO-US014832.
PF
XX
XX 10-MAY-2002; 2002US-0379831P.
PR
XX
XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
PA
XX Kier L, Nolan TD, Sankar U, Derbel M,
PI
XX MPI; 2004-042456/04.
DR
XX
XX Predicting the liver toxicity in an individual to an agent by measuring
PT the expression of one or more liver toxicity predictive genes in the
PT sample from the individual treated with the agent.
XX
XX Claim 7; Fig 4; 336pp; English.
XX
XX The present invention describes a method for predicting the liver
CC toxicity in an individual to an agent. The method comprises: (a)
CC obtaining a biological sample from the individual treated with the agent;
CC (b) measuring the expression of one or more liver toxicity predictive
CC genes in the sample; and (c) using the test expression profile with a set
CC of reference expression profiles in a Predictive Model to determine
CC whether the agent will induce liver toxicity in the individual. Also
CC described: (1) predicting the liver toxicity of an agent using an in
CC vitro system; (2) predicting the liver toxicity in a biological sample

CC from an individual, in vitro cell cultures or explants to an agent via a
CC programmable machine; (3) a computer program product for enabling a
CC computer to perform Predictive Model analysis for liver toxicity on a
CC biological sample from an individual, in vitro cell cultures or explants
CC to an agent; (4) a computer system adopted to predict liver toxicity in a
CC biological system from an individual, in vitro cell cultures or explants
CC to an agent; (5) a computer program product for predicting liver toxicity
CC from a test sample expression profile; (6) mining genes predictive of
CC liver toxicity; (7) an integrated system for predicting liver toxicity;
CC and (8) identifying one or more liver inflammation predictive genes. The
CC method is useful for predicting the liver toxicity in an individual to an
CC agent. The present sequence represents a liver toxicity predictive gene
CC sequence that represents a 24 hour combo 3 gene, which is specifically
CC claimed in the exemplification of the present invention.
XX
SQ Sequence 580 BP; 170 A; 129 C; 145 G; 125 T; 0 U; 11 Other;
Query Match 6.2%; Score 49.4; DB 12; Length 580;
Best Local Similarity 74.7%; Pred. No. 0.19;
Matches 62; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
OY 629 CCTGAAGAGAGAGCGCTCTCTTACTACACCATTTTACTTTCTTCTGAATTCATT 688
DB 494 CCTAAAGAGAGAGCGCTCTCTTACTACACCATTTTACTTTCTTCTGAATTCATT 435
OY 689 ACTTCTGTAGATAGTTCGT 711
DB 434 ACCTCTGTATATCATGTTCTTT 412
RESULT 44
ADR91158/c
ID ADR91158 standard; cDNA; 580 BP.
XX
XX ADR91158;
AC
XX 16-DEC-2004 (first entry)
DT
XX
XX Spleen necrosis predictive cDNA sequence, SEQ ID NO 114.
DE
XX altered expression; toxic response; spleen; toxicity; lymphoid; gene; ss.
XX
XX Unidentified.
OS
XX
XX MO2004083402-A2.
PN
XX 30-SEP-2004.
PD
XX
XX 17-MAR-2004; 2004MO-US008371.
PF
XX
XX 17-MAR-2003; 2003US-0455443P.
PR
XX
XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
PA
XX Sankar U, Kier L, Derbel M, Nolan T;
PI
XX MPI; 2004-691048/67.
DR
XX
XX New composition comprises cDNAs useful for detecting altered expression
PT of genes in a toxic response of the spleen or for predicting toxic
PT responses to one or more agents including lymphoid tissue types or other
PT species.
XX
XX Claim 1; SEQ ID NO 114; 249pp; English.
XX
XX The invention relates to a novel composition comprising cDNAs for use in
CC detecting the altered expression of genes in a toxic response of the
CC spleen, where the cDNAs comprises 50-816 base pairs (ADR91045-ADR91348)
CC or their complete complements. The invention further comprises:
CC monitoring the treatment of compound toxicity in a sample; predicting the
CC spleen toxicity in an individual to an agent; predicting the spleen
CC toxicity of an agent using an in vitro system; a computer program product
CC for predicting spleen toxicity from an expression profile of nucleic

CC acids from a sample under test, comprising a computer readable medium
CC bearing an encrypted training data set, encrypted lists of genes selected
CC from the cDNAs, and a predictive model for causing a general purpose
CC computer to predict the spleen toxicity of the sample based upon the
CC training data set, the list of genes selected from the cDNAs, and the
CC expression profile of nucleic acids from the sample; and an integrated
CC system for predicting spleen toxicity, comprising means for measuring
CC gene expression profiles of spleen predictive genes from samples exposed
CC to the test agent and a computer system operably linked to the means that
CC is capable of implementing a predictive model. The composition comprising
CC cDNAs is useful for detecting altered expression of genes in a toxic
CC response of the spleen or for predicting toxic responses to one or more
CC agents including lymphoid tissue types or other species. The predictive
CC genes and models of the invention are useful for identifying and
CC evaluating various in vitro systems that can be used to accurately
CC predict in vivo toxicity. This polynucleotide sequence represents one of
CC the genes predictive for spleen necrosis of the invention.
SQ Sequence 580 BP; 170 A; 129 C; 145 G; 125 T; 0 U; 11 Other;
Query Match 6.2%; Score 49.4; DB 13; Length 580;
Best Local Similarity 74.7%; Pred. No. 0.19;
Matches 62; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
Qy 629 CCGAAGAGAGAGGCTGCTTACTACACCATTTTACTTCTTCTGGAATTCATT 688
Db 494 CCTAAAGAGAGGCGCTGCTTACTACACCATTTTACTTCTTCTGGAATTCATT 435
Qy 689 ACTTCCTGTAGATTAATGTTCTGT 711
Db 434 ACCCTCTGTATATCAATGTTCTT 412
RESULT 45
ADB63776/C
ID ADB63776 standard; cDNA; 2372 BP.
XX
AC ADB63776;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human cDNA encoding clone UTERU20065470.
XX
KW Human; ss; gene; pharmaceutical; diagnostic; gene therapy;
KW tissue regeneration; cell regeneration; membrane protein;
KW signal transduction-related protein; transcription-related protein;
KW osteoporosis; neurological disease; cancer; tumour.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 389..694
FT FT /*cag= a
FT FT /product= "Clone UTERU20065470 protein"
XX
XX EPI308459-A2.
XX
XX 07-MAY-2003.
XX
PF 28-MAR-2002; 2002EP-00007401.
XX
PR 05-NOV-2001; 2001JP-00379298.
PR 25-JAN-2002; 2002US-00350978.
XX
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Iisogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I,
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Maehuo Y,
XX WPI; 2003-450961/43.
DR P-PSDB; ADB65746.

XX
PT New polynucleotides and polypeptides, useful for developing a diagnostic
PT marker or medicines for regulation of their expression and activity, or
PT as targets of gene therapy.
PS Claim 1; Page; 222pp; English.
XX
CC The invention discloses a polynucleotide comprising a sequence selected
CC from 1970 fully defined nucleotide sequences which encode novel
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC or its partial peptide, an antibody binding to the polypeptide or peptide
CC of the polynucleotide, immunologically assaying the polypeptide or
CC peptide of the polynucleotide by contacting the polypeptide or peptide
CC with the antibody of the encoded protein, and observing the binding
CC between the two, a transformant carrying the polynucleotide in an
CC expressible manner and an antisense polynucleotide. The oligonucleotide
CC is useful as a primer for synthesizing the polynucleotide, or as a probe
CC for detecting the polynucleotide. The polynucleotides and encoded
CC proteins are useful as pharmaceutical agents and many disease-related
CC genes may be included in them, for developing a diagnostic marker or
CC medicines for regulation of their expression and activity, or as targets
CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a cDNA of the invention. Note: Some of the sequence
CC data for this patent is not represented in the printed specification, but
CC is based on sequence information supplied by the European Patent Office.
XX
SQ Sequence 2372 BP; 682 A; 440 C; 486 G; 764 T; 0 U; 0 Other;
Query Match 6.1%; Score 48.8; DB 10; Length 2372;
Best Local Similarity 70.7%; Pred. No. 0.35;
Matches 65; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
Qy 626 GTACCTGAAGAGAGGCTGCTTACTACACCATTTTACTTCTTCTGGAATTC 685
Db 1382 GCACCTTAAGAGAGGCTGCTGCCCCGATTAATCTTCATTTGTTCTCTCCAGATTC 1323
Qy 686 ATTACTTCTGTAGATTAATGTTCTGTAGAAA 717
Db 1322 ATAACTTCTTATATATCATTTCTGTAAAGA 1291
RESULT 46
ADJ64020/C
ID ADJ64020 standard; DNA; 1765 BP.
XX
AC ADJ64020;
XX
DT 06-MAY-2004 (first entry)
XX
DE DNA sequence encoding JNK2 protein.
XX
KW C-Jun N-terminal kinase; cytosolic; immunosuppressive; dermatological;
KW antiinflammatory; cardiac; antirheumatic; antiarthritic; anti-HIV;
KW respiratory; Gen; antiparasitic; vasodilator; antibacterial; antihypertensive;
KW cancer; colon cancer; renal cell carcinoma; prostate cancer;
KW non-small cell carcinoma; psoriasis; pemphigus vulgaris;
KW Behcet's syndrome; acute respiratory distress syndrome; ARDS;
KW ischaemic heart disease; post-dialysis syndrome; leukaemia;
KW rheumatoid arthritis; AIDS; vasculitis; septic shock; inflammation;
KW lipid histiocytosis; JNK; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 59..1333
FT FT /*cag= a
FT FT /product= "JNK2 protein"

PN US2003190735-A1.
XX
XX 09-OCT-2003.
XX
PF 18-MAY-2001; 2001US-00861012.
XX
PR 19-JUL-1993; 93US-00094533.
PR 25-MAR-1994; 94US-00220602.
PR 18-JUL-1994; 94US-00276860.
PR 19-MAY-1995; 95US-00444393.
PR 13-FEB-1997; 97US-00799913.
PR 08-SEP-1998; 98US-00150201.
PR 14-DEC-1999; 99US-00461649.
XX
XX (KARI/) KARIN M.
XX (HIBI/) HIBI M.
XX (LINA/) LIN A.
PI Karin M, Hibi M, Lin A;
XX
XX WPI; 2003-844275/78.
XX P-PSDB; ADJ64021.
XX
XX
XX New polynucleotide encoding a c-Jun N-terminal kinase (JNK), and the
PT encoded polypeptide, useful for (identifying compounds for) treating e.g.
PT cancer, psoriasis, rheumatoid arthritis, or septic shock.
XX
XX Claim 7; SEQ ID NO 17; 50pp; English.
XX
XX This invention relates to a novel polynucleotide encoding a c-Jun N-
CC terminal kinase that phosphorylates the c-Jun N-terminal activation
CC domain. The polynucleotide sequence of the invention may have cytostatic,
CC immunosuppressive, dermatological, anti-inflammatory, cardiant,
CC antirheumatic, antiarthritic, anti-HIV, respiratory-gen, antipsoriatic,
CC vasotropic, antibacterial, antileukemic activities. Also disclosed in the
CC invention are modulators of the activity or expression of the c-Jun N-
CC terminal kinase (JNK) such as competitive inhibitor peptides, antibodies,
CC and sense or antisense polynucleotides which are useful for treating cell
CC proliferative disorders associated with JNK. These include cancers such
CC as colon cancer, renal cell carcinoma, prostate cancer, and non-small
CC cell carcinoma, and non-malignant or immunological-related cell
CC proliferative diseases, such as psoriasis, pemphigus vulgaris, Behçet's
CC syndrome, acute respiratory distress syndrome (ARDS), ischemic heart
CC disease, post-dialysis syndrome, leukemia, rheumatoid arthritis, AIDS,
CC vasculitis, septic shock, and other types of inflammation or lipid
CC histiocytosis. The polypeptide of the invention may be useful in a
CC screening method for identifying molecules which modulate its activity
CC which are potentially useful as therapeutics. The present sequence
CC represents a DNA sequence encoding the JNK2 protein used in the
XX exemplification of the invention.
XX
SQ Sequence 1765 BP; 539 A; 356 C; 396 G; 474 T; 0 U; 0 Other;
Query Match 6.0%; Score 48.4; DB 10; Length 1765;
Best Local Similarity 74.4%; Pred. No. 0.41; Mismatches 0; Gaps 0;
Matches 61; Conservative 0; Indels 21; Indels 0; Gaps 0;
QY 630 CTGAGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTTCTTGAATTCATTA 689
DB 1196 CTGCATCTGAGAGGCTGATCTTTTACACACCATTTGCTTCTTCCCATTCATGA 1137
QY 690 CTTCCTTGATGATTAAGTTCGT 711
DB 1136 CTTCCTTGATTAATTAAGTCTTT 1115

DT 13-OCT-1995 (first entry)
XX
XX JNK2 Oncoprotein polypeptide kinase coding sequence.
DE
XX
XX Oncoprotein; polypeptide kinase; JNK; c-Jun; AP-1; leukemia;
KM prostate cancer; lung cancer; colon cancer; se.
XX
XX Homo sapiens.
OS
XX
XX Key location/Qualifiers
FH 59.1336
FT CDS /*tag= a
FT /product= "Oncoprotein protein kinase."
XX
XX WO9503323-A1.
XX
XX 02-FEB-1995.
XX
XX 18-JUL-1994; 94WO-US008119.
XX
XX 19-JUL-1993; 93US-00094533.
XX 25-MAR-1994; 94US-00220602.
XX
XX (REGC) UNIV CALIFORNIA.
PA (UYMA-) UNIV MASSACHUSETTS MEDICAL SCHOOL.
XX
XX Karin M, Davis R, Hibi M, Lin A, Derjard B;
XX
XX WPI; 1995-075186/10.
XX P-PSDB; AAR70768.
XX
XX
XX Onco/protein protein kinase, JNK - useful for regulating c-Jun activity
PT and gene expression in cells.
XX
XX Claim 57; Fig 28; 143pp; English.
XX
XX JNK1 (See AAR70767) and JNK2 phosphorylate the c-Jun N-terminal
CC activation domain which affect gene expression from AP-1 sites. The 2
CC protein kinases allow the detection of the level of specific kinase
CC activity associated with activation of c-Jun and AP-1. Cell proliferative
CC disorders associated with JNK can be treated by administering a
CC therapeutically effective amount of a reagent which modulates JNK
CC activity. Disorders such as leukemia, cancers of prostate, lung (non-
CC small cell) and colon. (updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 1780 BP; 541 A; 363 C; 402 G; 474 T; 0 U; 0 Other;
Query Match 6.0%; Score 48.4; DB 2; Length 1780;
Best Local Similarity 74.4%; Pred. No. 0.41; Mismatches 0; Gaps 0;
Matches 61; Conservative 0; Indels 21; Indels 0; Gaps 0;
QY 630 CTGAGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTTCTTGAATTCATTA 689
DB 1196 CTGCATCTGAGAGGCTGATCTTTTACACACCATTTGCTTCTTCCCATTCATGA 1137
QY 690 CTTCCTTGATGATTAAGTTCGT 711
DB 1136 CTTCCTTGATTAATTAAGTCTTT 1115

RESULT 48
ADA26313/C
ID ADA26313 standard; cDNA; 1780 BP.
XX
XX ADA26313;
XX
XX 20-NOV-2003 (first entry)
XX
XX cDNA encoding c-Jun N-terminal kinase 2, JNK2.
XX
XX immunological disorder; non-malignant cell-proliferative disorder;
XX leukemia; organ related malignancy; acute inflammation;
XX c-Jun N-terminal kinase 2; JNK 2; immunopathological disorder;
KM

KW	septic shock; acute respiratory distress syndrome; ARDS; AIDS;
KM	rheumatoid arthritis; psoriasis; pemphigus vulgaris;
KV	ischemic heart disease; leukaemia; post dialysis disorder; vasculitis;
XX	ss; gene.
OS	Unidentified.
XX	
FH	Key Location/Qualifiers
FT	CD5 59..1333
FT	/tag= a
XX	/Product= "JNK2"
PN	
PD	US2002192218-A1.
XX	
PF	19-DEC-2002.
XX	
PR	18-MAY-2001; 2001US-00861097.
XX	
PR	19-JUL-1993; 93US-00094533.
XX	
PR	25-MAR-1994; 94US-00220602.
XX	
PR	18-JUL-1994; 94US-00276860.
XX	
PR	19-MAY-1995; 95US-00444393.
XX	
PR	13-FEB-1997; 97US-00799913.
XX	
PR	08-SEP-1998; 98US-00150201.
XX	
PA	14-DEC-1999; 99US-00461649.
XX	
PA	(KARI/) KARIN M.
XX	(HIBI/) HIBI M.
PA	(LINA/) LIN A.
XX	
PI	Karin M, Hibi M, Lin A;
DR	
XX	WPI: 2003-596375/56.
DR	P-PsDB; ADA26314.
XX	
PT	Treating immunological disorder, non-malignant cell-proliferative
PT	disorder, organ related malignancy or acute inflammation, associated with
PT	c-Jun N-terminal kinase, by giving a compound which modulates kinase
PT	activity.
XX	
PS	Example 23; Page 32-34; 47pp; English.
XX	
CC	The invention relates to a method of treating an immunological disorder,
CC	non-malignant cell-proliferative disorder, leukaemia, an organ related
CC	malignancy or acute inflammation, associated with c-Jun N-terminal kinase
CC	(JNK), comprising administering to a subject, a compound which modulates
CC	the kinase activity. The method is useful for treating an immunological
CC	disorder, non-malignant cell-proliferative disorder, leukaemia, an organ
CC	related malignancy and acute inflammation. The disorder is associated
CC	with immunological disorder is an immunopathological disorder and is
CC	related to acute inflammation or septic shock, or the disorder is acute
CC	respiratory distress syndrome (ARDS), AIDS or rheumatoid arthritis. The
CC	disorder associated with non-malignant cell-proliferative disorder is
CC	psoriasis, pemphigus vulgaris, ischemic heart disease, leukemia, post
CC	dialysis disorder and vasculitis. In organ related malignancy, the organ
CC	is the lymphoid system, breast, gastrointestinal system or genito-urinary
CC	tract. The present sequence represents cDNA encoding c-Jun N-terminal
CC	kinase 2, JNK2.
XX	
SQ	Sequence 1780 BP; 541 A; 359 C; 402 G; 478 T; 0 U; 0 Other;
XX	
Query March	6.0%; Score 48.4; DB 9; Length 1780;
Best Local Similarity	74.4%; Pred No. 0.41;
Matches 61; Conservative	0; Mismatches 21; Indels 0; Gaps 0;
OY	630 CTGAAGGAAAGCTGTCCTTTACTACACCATTATTAAGTCTTTCTTGATTCATTA 689
Dd	1196 CTGCATCTGAAGGTGCATCTTTACAACCACTTCTGCTTCTTCCCATCACA 1137
OY	690 CTCCTTGATAGTAGTTCTGT 711
Dd	1136 CTCCTTGATAGTAGTTCTTT 1115

RESULT 49
ID AC62801/c
AC62801 standard; DNA; 1780 BP.
XX
XX ACAA2801;
DT 21-AUG-2003 (first entry)
XX
DE Human c-Jun N-terminal kinase, JNK2, CDNA.
XX
KW Human; JNK2; cell proliferative disorder; serine kinase; ss; gene;
KW threonine kinase; psoriasis; pemphigus vulgaris; Behcet's syndrome;
KW acute respiratory distress syndrome; ARDS; ischaemic heart disease;
KW leukaemia; rheumatoid arthritis; AIDS; vasculitis; septic shock; cancer;
KW c-Jun N-terminal kinase.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 59..133
FT /tag=
FT /product= "JNK2"
PN US2003044788-A1.
XX
PD 06-MAR-2003.
XX
PF 18-MAY-2001; 2001US-00861098.
XX
PR 19-JUL-1993; 93US-00094533.
PR 25-MAR-1994; 94US-00220602.
PR 18-JUL-1994; 94US-00276860.
PR 19-MAY-1995; 95US-00443393.
PR 13-FEB-1997; 97US-00799913.
PR 08-SEP-1998; 98US-00150201.
PR 14-DEC-1999; 99US-00461649.
XX
PA (KARI/) KARIN M.
PA (HIBI/) HIBI M.
PA (LINAI/) LIN A.
XX
PI Karin M, Hibl M, Lin A;
DR WP1: 2003-479738/45.
P-PSDB; ABU62138.
XX
PT Identifying a composition useful to treat a cell proliferative disorder,
PT comprises incubating the composition and a serine/threonine kinase or
PT polynucleotide encoding the kinase and measuring the effect of the
PT composition on the kinase.
XX
PS Claim 3; Page 32-34; 50pp; English.
XX
CC The invention relates to a method of identifying a composition useful for
CC treating a proliferative disorder, affecting a kinase having serine and
CC threonine kinase activity and phosphorylating a c-Jun N-terminal
CC activation domain. The method is useful for identifying a composition
CC which is useful for treating a cell proliferative disorder, where the
CC effect is inhibition or stimulation of the kinase, and the composition is
CC an immunosuppressing agent. The composition identified by the above
CC method, is useful for treating a cell proliferative disorder e.g. cancer,
CC psoriasis, pemphigus vulgaris, Behcet's syndrome, acute respiratory
CC distress syndrome (ARDS), ischaemic heart disease, leukaemia, rheumatoid
CC arthritis, AIDS, vasculitis and septic shock. The present sequence
CC represents the human c-Jun N-terminal kinase, JNK2, CDNA
XX
SQ Sequence 1780 BP; 541 A; 359 C; 402 G; 478 T; 0 U; 0 Other;
Query Match 6.0%; Score 48.4; DB 9; Length 1780;
Best Local Similarity 74.4%; Pred. No. 0.41;
Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGGCTGCTCTTTACTACACATTTTGTCTTTCTTGAATTCATTA 689
 DB 1196 CTGCATCTGAAGGCTGATCTTTTACACACATTTGCTTCTTCTCCCAATCCATGA 1137
 QY 690 CTTCCTTGATAGATAGTCTGT 711
 DB 1136 CTTCCTTGATAGATAGTCTGT 1115

RESULT 50

AAA48656/c

ID AAA48656 standard; DNA; 1782 BP.

AC AAA48656;

DT 20-SEP-2000 (first entry)

DE Human JNK2 DNA.

XX Antisense; E-selectin; TNF alpha; cell adhesion; human;
 KM tumour necrosis factor alpha; phosphorothioate; methoxyethoxy; sepsis;
 KM rheumatoid arthritis; inflammatory; immune disease;
 KM inflammatory bowel disease; allergic contact dermatitis; psoriasis;
 KM diabetes; Grave's disease; allograft rejection; cancer; antibacterial;
 KM immunosuppressive; antipsoriatic; antidiabetic; antithyroid; cytostatic;
 KM dermatological; antiallergic; Ha-ras; c-raf; c-Jun N-terminal kinase;
 KM JNK; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 59..1333
 FT /*tag= a
 FT /product= "JNK2"

PN W0200034303-A1.

PD 15-JUN-2000.

PF 08-DEC-1999; 99W0-US028965.

PR 10-DEC-1998; 98US-00209668.

PA (ISIS-) ISIS PHARM INC.

PI Monia BP, Xu XS;

DR WPI; 2000-423367/36.

DR P-PSDB; AAY94503.

PT Modulating cell adhesion molecule expression for treating immune or
 PT inflammatory diseases involves treating cell with specific inhibitor of
 PT Tumor Necrosis Factor alpha signaling molecule.

PS Example 2; Page 88-90; 100pp; English.

CC A novel method for modulating cell adhesion molecule expression involves
 CC antisense inhibition of a tumour necrosis factor (TNF) alpha signaling
 CC molecule. In the method TNF alpha signaling molecules Ha-ras, c-raf and
 CC c-Jun N-terminal kinase (JNK)2 were inhibited by antisense
 CC oligonucleotides. In addition an antisense oligonucleotide to the cell
 CC adhesion molecule E-selectin was also examined. The present sequence is
 CC human JNK2 DNA. This sequence was used to generate the JNK2 antisense
 CC oligonucleotide. The antisense oligonucleotides used in the method
 CC contained modifications, namely phosphorothioate linkages and
 CC 2-methoxyethoxy bases. Some C residues also had a 5' methyl modification.
 CC Inhibitors of the TNF alpha signalling molecules have antibacterial,
 CC immunosuppressive, antipsoriatic, antidiabetic, antithyroid, cytostatic,
 CC dermatological, antiallergic and antiinflammatory activity. The antisense
 CC inhibitors may be useful for the treatment of sepsis, rheumatoid
 CC arthritis, inflammatory, immune disease, inflammatory bowel disease,
 CC allergic contact dermatitis, psoriasis, diabetes, Grave's disease,
 CC allograft rejection and cancer

XX SQ Sequence 1782 BP; 541 A; 359 C; 404 G; 478 T; 0 U; 0 Other;
 SQ Query Match 6.0%; Score 48.4; DB 3; Length 1782;
 SQ Best Local Similarity 74.4%; Pred. No. 0.41; 21; Indels 0; Gaps 0;
 SQ Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGGCTGCTCTTTACTACACATTTTGTCTTTCTTGAATTCATTA 689
 DB 1196 CTGCATCTGAAGGCTGATCTTTTACACACATTTGCTTCTTCTCCCAATCCATGA 1137
 QY 690 CTTCCTTGATAGATAGTCTGT 711
 DB 1136 CTTCCTTGATAGATAGTCTGT 1115

Search completed: July 19, 2006, 18:53:02
 Job time : 658 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2006, 18:42:15 ; Search time 4914 Seconds
(without alignments)
9103.676 Million cell updates/sec

Title: US10723681MOD.SEQ

Perfect score: 800

Sequence: 1 acatttcctcaactctta.....caataatcgttcgacg 800

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

EST.*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	397.8	49.7	401	11	AQ046186
C 2	293.2	36.6	393	11	AQ129390 HS 3045_A
C 3	82.8	10.3	247	2	BG204609
C 4	82.8	10.3	380	4	CB069799
C 5	82.8	10.3	407	2	BF856752
C 6	82.8	10.3	449	7	AM297251 UI-H-BW0
C 7	82.8	10.3	448	1	AA663771
C 8	82.8	10.3	512	3	BM704479 UI-B-CK1
C 9	82.8	10.3	595	2	BM508552
C 10	82.8	10.3	605	5	CK825957
C 11	82.8	10.3	618	3	BQ287873
C 12	82.8	10.3	921	10	DR762335
C 13	82.8	10.3	932	4	BI824308
C 14	81.8	10.2	462	4	BX282592
C 15	80.4	10.1	315	2	BF851981
C 16	80.4	10.1	386	2	BF858136
C 17	80.4	10.1	457	4	CB069160
C 18	80.4	10.1	789	2	BG194386
C 19	78.8	9.8	257	2	BG209408

C 20	78	9.8	836	5	CJ443965	CJ443965
C 21	77.2	9.7	263	5	CR659197	CR659197
C 22	76.4	9.6	946	5	CF408692	CF408692
C 23	75.6	9.4	818	5	CJ491725	CJ491725
C 24	75.4	9.2	568	9	DA807178	DA807178
C 25	73.2	9.4	408	2	BF857793	BF857793
C 26	70	8.8	423	7	AM314598	AM314598
C 27	70	8.8	708	9	DN543033	DN543033
C 28	69.6	8.7	300	7	BE752856	BE752856
C 29	69.6	8.7	351	7	BE752856	BE752856
C 30	69	8.6	916	10	DV915213	DV915213
C 31	68.8	8.6	332	4	BE56616	BE56616
C 32	68.4	8.6	543	7	BE562295	BE562295
C 33	68.4	8.6	543	3	BU733848	BU733848
C 34	68.4	8.6	763	3	CB234404	CB234404
C 35	68.4	8.6	2343	6	AK042368	AK042368
C 36	68.4	8.6	2729	6	AK036275	AK036275
C 37	67.8	8.5	561	2	BF854904	BF854904
C 38	67.8	8.4	2629	6	AK163206	AK163206
C 39	67	8.3	576	4	CB607972	CB607972
C 40	66.8	8.2	570	5	CF535846	CF535846
C 41	66	8.2	578	3	BM944347	BM944347
C 42	66	8.2	639	8	CF951683	CF951683
C 43	66	8.2	721	5	CF951683	CF951683
C 44	66	8.2	721	5	BM943588	BM943588
C 45	66	8.2	802	9	CK852086	CK852086
C 46	66	8.2	802	9	CK852086	CK852086
C 47	64.4	8.1	642	3	BP485311	BP485311
C 48	64	8.0	331	3	BU389929	BU389929
C 49	59	7.4	720	2	BU725204	BU725204
C 50	55.8	7.0	645	8	CX143962	CX143962
C 51	55.8	7.0	646	8	CX143962	CX143962
C 52	55.8	7.0	733	10	DT231368	DT231368
C 53	54	6.8	743	5	CK638880	CK638880
C 54	54	6.8	825	1	AF064929	AF064929
C 55	54	6.8	1284	14	AY411698	AY411698
C 56	54	6.8	2590	6	AK139498	AK139498
C 57	53.2	6.7	1060	14	CNS0047R	CNS0047R
C 58	52.8	6.6	425	2	BU720556	BU720556
C 59	51.8	6.5	801	14	BX142194	BX142194
C 60	51.6	6.5	500	5	CD803749	CD803749
C 61	51.6	6.5	652	4	CA324408	CA324408
C 62	51.6	6.5	654	7	BB253136	BB253136
C 63	51.6	6.5	1466	6	AK043102	AK043102
C 64	51	6.4	948	14	CNS0171M	CNS0171M
C 65	50.8	6.3	697	4	CA057984	CA057984
C 66	50.8	6.3	708	7	AW914916	AW914916
C 67	50.8	6.3	928	14	CNS000DKY	CNS000DKY
C 68	50.8	6.3	1167	14	CNS007360	CNS007360
C 69	50	6.2	763	2	BM414648	BM414648
C 70	50	6.2	784	5	CK637229	CK637229
C 71	50	6.2	801	2	BI820604	BI820604
C 72	49.8	6.2	987	14	CNS014PQ	CNS014PQ
C 73	49.8	6.2	1092	14	CNS020X7	CNS020X7
C 74	49	6.1	1101	14	CNS0039G	CNS0039G
C 75	48.8	6.1	928	14	CNS000DKY	CNS000DKY
C 76	48.4	6.0	324	1	AA251965	AA251965
C 77	48.4	6.0	458	3	BM689515	BM689515
C 78	48.4	6.0	465	3	BO187463	BO187463
C 79	48.4	6.0	496	10	H16067	H16067
C 80	48.4	6.0	496	10	BX282296	BX282296
C 81	48.4	6.0	565	9	DA405535	DA405535
C 82	48.4	6.0	571	9	DA195866	DA195866
C 83	48.4	6.0	572	3	BO185526	BO185526
C 84	48.4	6.0	592	7	AW502260	AW502260
C 85	48.4	6.0	686	14	CR914758	CR914758
C 86	48.4	6.0	697	7	CF787382	CF787382
C 87	48.4	6.0	704	8	CN164573	CN164573
C 88	48.4	6.0	714	1	AL119951	AL119951
C 89	48.4	6.0	754	3	CR549979	CR549979
C 90	48.4	6.0	759	3	BU852625	BU852625
C 91	48.4	6.0	764	14	CT237644	CT237644
C 92	48.4	6.0	942	1	AL539761	AL539761

C 93 48.4 6.0 1033 1 AJ927386
C 94 48.4 6.0 1101 14 CNS00807
C 95 48.4 6.0 1118 4 BX403747
C 96 47.8 6.0 754 1 AQ951683
C 97 47.6 6.0 512 14 CR339134
C 98 47.6 6.0 660 14 CR466489
C 99 47.6 6.0 897 12 CG933873
C 100 47.4 5.9 251 1 AA333513

ALIGNMENTS

RESULT 1
LOCUS AQ046186/c 401 bp DNA linear GSS 14-Apr-1999
DEFINITION Rpci11-31H10.TV Rpci-11 Homo sapiens genomic clone Rpci-11-31H10,
genomic survey sequence.
ACCESSION AQ046186
VERSION AQ046186.1 GI:3315113
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 401)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
Venter,J.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@igf.org

Clones are derived from the human BAC library Rpci-11. For BAC
library availability, please contact Pieter de Jong
(pieterdejong.med.bufiled.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.bufiled.edu/ordering>) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.cigr.org/cdb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..401
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7511697"
/db_xref="taxon:9606"
/clone="Rpci-11-31H10"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="Rpci-11"
/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;
Rpci11 Human Male BAC Library"

ORIGIN

Query Match 49.7%; Score 397.8; DB 11; Length 401;
Best Local Similarity 99.5%; Pred. No. 1.2e-80;
Matches 399; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 280 AGATTACTGAGCTCCACATTTGACTGATGCTCAAAAGGCAATTGCTGCAATTTG 339
DB 401 AGATTACTGAGCTCCACATTTGACTGATGCTCAAAAGGCAATTGCTGCAATTTG 342
QY 340 ATGAGGACATTTACCTTTAGCCCATGTTAACAATTTCTTGAGATTCATTTCTA 399
DB 341 ATGAGGACATTTACCTTTAGCCCATGTTAACAATTTCTTGAGATTCATTTCTA 282
QY 400 AATTATTATGAAAAAGTTTGTCTGATCATTCATTCAGATTAATGATGATGATG 459

DB 281 AATTATTATGAAAAAGTTTGTCTGATCATTCATTCAGATTAATGATGATGATG 222
QY 460 CCACACTGATATTCAGAGAAATTAATCAATTCATTAAGACACACATGATGATA 519
DB 221 CCACACTGATATTCAGAGAAATTAATCAATTCATTAAGACACACATGATGATA 162
QY 520 TTGTGTCATCTGCTTTTAAAGCAATGTTATTTCTTGCAACCCCTACCAAGGCC 579
DB 161 TTGTGTCATCTGCTTTTAAAGCAATGTTATTTCTTGCAACCCCTACCAAGGCC 102
QY 580 AAGAAATTACACAGACTAGTTATTTGTTATTCACGAGAGTACTGAGAGAGA 639
DB 101 AAGAAATTACACAGACTAGTTATTTGTTATTCACGAGAGTACTGAGAGAGA 42
QY 640 AGGCTGCTCTTTTACTACACCAATTTTACTCTTTCTCTG 680
DB 41 AGGCTGCTCTTTTACTACACCAATTTTACTCTTTCTCTG 1

RESULT 2
LOCUS AQ129390/c 393 bp DNA linear GSS 23-SEP-1998
DEFINITION HS 3045 A2 F04 MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3045 Col=8 Row=K, genomic survey
sequence.
ACCESSION AQ129390
VERSION AQ129390.1 GI:3506556
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 393)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3045 Row: K Column: 8
Class: BAC ends
High quality sequence stop: 393.

FEATURES

source

Location/Qualifiers

1..393
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3045 Col=8 Row=K"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"

ORIGIN

Query Match 36.6%; Score 293.2; DB 11; Length 393;
Best Local Similarity 91.7%; Pred. No. 1.3e-56;
Matches 321; Conservative 0; Mismatches 28; Indels 1; Gaps 1;
QY 331 TGAATTGATGAGGACATTT-TACCCTTGCCCATGTTAATTTCTTGAGATTTCA 389
DB 330 TCAATTGTATCAGGACATTTACTCCATATGACCATGTGACATATTTGTTCAAGATTCA 291

QY 390 TTACTATTAATTAATTATGAAAAAGTTTTCCTGATCATTTACCATCAGAAATATC 449
 DB 290 TTACTATTAAGTCAATATATTAAGTTTCTGATGATCATTTCAATTCAGATATATC 231
 QY 450 AGAATGATGACACACTGAAATATCAAAAAGAAATATAATCATTTATTAAGACACAA 509
 DB 230 AGAATGATGACACAAATGAAATATCAAGAAATATGAACTAAAGTCATTAAGACACAA 171
 QY 510 CCATGATATATTTTCCATCTGCTCTTTTAAAGCAATGTTATGTTATTTCTTGCAACCCCTA 569
 DB 170 CCAATGATATATTTTCCATCTGCTCTTTTAAAGCAATGTTATGTTATTTCTTGCAACCCCTA 111
 QY 570 CACAAAGCCCAAGAAATTAACAAGTACTATTGTTATGTTATTAAGACAGAGATAC 629
 DB 110 CACAAAGCCCAAGAAATTAACAAGTACTATTGTTATGTTATTAAGACAGAGATAC 51
 QY 630 CTGAAGAGAGAGGCTGCTCTTTTACTACACATTTTACTTTCTTCT 679
 DB 50 CTGAAGAGAGAGGCTGCTCTTTTACTACACATTTTACTTTCTTCT 1

RESULT 3
 BC204609/c 247 bp mRNA linear EST 21-APR-2001
 LOCUS RST24016 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.
 DEFINITION BC204609
 ACCESSION BC204609.1 GI:13726296
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 247)
 Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramchandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Kikka, A., Hess, J., Cochren, K., Lo, K., Offenbacher, J., Danzig, J., and Ducar, M.
 Creation of genome-wide protein expression libraries using random activation of gene expression
 Nat. Biotechnol. 19 (5), 440-445 (2001)
 11329013
 JOURNAL
 PUBMED
 COMMENT
 Contact: Scott J. Cain
 Atherys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scain@atherys.com
 High quality sequence stop: 197.
 Location/Qualifiers
 1. 247
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cell_line="HT1080"
 /clone_lib="Atherys RAGE Library"
 /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
 ORIGIN
 Query Match 10.3%; Score 82.8; DB 2; Length 247;
 Best Local Similarity 97.7%; Pred. No. 2.8e-08;
 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 626 GTACTGAAGAGAGGCTGCTCTTTTACTACACATTTTACTTTCTTCTGAATTC 685
 DB 150 GCACCTGAAGAGAGGCTGCTCTTTTACTACACATTTTACTTTCTTCTGAATTC 91

QY 686 ATTACTCTCTTGAGTAAGTTCTGT 711
 DB 90 ATTACTCTCTTGAGTAAGTTCTTT 65

RESULT 4
 CB069799/c 390 bp mRNA linear EST 21-JAN-2003
 LOCUS 1829B07.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6553861 5
 DEFINITION similar to SW:MK10_HUMAN P53779 MITOGEN-ACTIVATED PROTEIN KINASE 10
 / mRNA sequence.
 ACCESSION CB069799
 VERSION CB069799.1 GI:27814319
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 390)
 Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Maira, M., Page, D., Wylie, T., Martin, J., Blistein, A., Schmitt, A., Treising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Teagareitvilli, R., Williams, T., Jackson, Y. and Bowers, Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Other ESTs: 1829B07.x1
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Dr. Hiroshi Inoue
 (hinoue@im.wustl.edu)
 Seq primer: -40UP from Gibco
 High quality sequence stop: 345.
 Location/Qualifiers
 1. 390
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6553861"
 /cissue_type="Purified pancreatic islet"
 /clone_lib="HR85 islet"
 /lab_host="DH10B"
 /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
 ORIGIN
 Query Match 10.3%; Score 82.8; DB 4; Length 390;
 Best Local Similarity 97.7%; Pred. No. 2.9e-08;
 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 626 GTACTGAAGAGAGGCTGCTCTTTTACTACACATTTTACTTTCTTCTGAATTC 685
 DB 138 GCACCTGAAGAGAGGCTGCTCTTTTACTACACATTTTACTTTCTTCTGAATTC 79
 QY 686 ATTACTCTCTTGAGTAAGTTCTGT 711

Db 78 ATTACTCTGTGATGATGATCTTT 53

RESULT 5
LOCUS BF856752/c 407 bp mRNA linear EST 16-JAN-2001
DEFINITION QV1-F10202-021100-455-f02 F10202 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF856752
VERSION BF856752.1 GI:12244496
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 407)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jorgensen, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
JOURNAL
PUBMED
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL:
(http://www.ludwig.org.br/scripts/gethtml.pl?pl=QV1&f2=QV1-F10202-021100-455-f02&f3=2000-11-02&f4=1)
Seq primer: puc 18 forward
High quality sequence stop: 407.
Location/Qualifiers
1. 407
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="F10202"
/note="Organ: prostate tumor; Vector: puc18; Site: 1; Smal; Site 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
ORIGIN
Query Match 10.3%; Score 82.8; DB 2; Length 407;
Best Local Similarity 97.7%; Pred. No. 2.9e-08;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GTACCGAAGGAGGCGTCTTTTACACCATTTTACTCTTTCTTGTAATTC 685
Db 99 GCACCGAAGGAGGCGTCTTTTACACCATTTTACTCTTTCTTGTAATTC 40
QY 686 ATTACTCTGTGATGATGATCTTT 711
Db 39 ATTACTCTGTGATGATGATCTTT 14
RESULT 6
LOCUS AM297251/c 429 bp mRNA linear EST 16-JAN-2000
DEFINITION UI-H-BW0-aj1-b-12-0-UI.61 NCI_CGAP_sub6 Homo sapiens cDNA clone

IMAGE:2731750 3', mRNA sequence.
AM297251
DEFINITION UI-H-BW0-aj1-b-12-0-UI.61 NCI_CGAP_sub6 Homo sapiens cDNA clone
ACCESSION AM297251.1 GI:6703887
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 429)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
JOURNAL
PUBMED
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA library preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: www.bio.lnlnl.gov/birop/image/image.html
Seq primer: M13 Forward
POLY:A=yes.
Location/Qualifiers
1. 429
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2731750"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Sub6"
/note="Vector: pT7T3D-Pac1; Site 1: Not I; Site 2: Eco RI; NCI CGAP Sub6 is a subcloned library derived from BW, which consists of a mixture of four normalized libraries: NCI CGAP Brn50, NCI CGAP Lu13, NCI CGAP Ovi8, GBC1. The NCI CGAP Sub6 library had 7 million recombinants. A single-stranded DNA preparation of BW was used as a tracer in a subtractive hybridization with a driver comprising: the IMAGE pool (NCI CGAP Kid3 pool 1, LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE Clonoids 1322376-1323911, 1456008-1456775, 1500552-1502855); NCI CGAP Kid5 pool 1, LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonoids 1323912-1325831, 1471368-1472903, 1492104-1493253); NCI CGAP Lu5 pool 1, LLAM 3575-3582, 3651-3854 (IMAGE Clonoids 1414920-1417991, 1520904-1522439); NCI CGAP GC4 pool 1, LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clonoids 1257096-1258631, 1469064-1470983, 1475992-1476743); NCI CGAP Pr22 pool 1, LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonoids 985608-986759, 1101192-1101959, 1217928-1220615); NCI CGAP Colo pool 1, LLAM 2644-2653, 2871-2872 (IMAGE Clonoids 1057416-1061255, 1144584-1145351). (50% of the driver population), plus a pool of 3,840 arrayed clones from NCI CGAP Sub1 (IMAGE Clonoids 2708616-2710535) and NCI CGAP Sub2 (IMAGE Clonoids 2710536-2712455) and (20% of the driver population), plus a pool of 11,136 clones from NCI CGAP Sub3 (IMAGE Clonoids 2712456-2713591) (30% of the driver population). Subtraction was performed as previously described [Bonaldi, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806. TAG_LIB=NCI CGAP-Lu13
TAG_SEQ=GCCGG"
ORIGIN
Query Match 10.3%; Score 82.8; DB 7; Length 429;
Best Local Similarity 97.7%; Pred. No. 2.9e-08;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GTACCGAAGGAGGCGTCTTTTACACCATTTTACTCTTTCTTGTAATTC 685

```

Db      291 GCACCTGAAGAGAGGCTGCTCTTACTACTACACCATTTTACTTTCTTCGAAATTC 232
|-----|
Qy      686 ATTACTCTCTGTAGATAGTTCTGT 711
|-----|
Db      231 ATTACTCTCTGTAGATAGTTCTTT 206
|-----|

RESULT 7
LOCUS   AA663771
DEFINITION ae68h10.s1 StrataGene schizo brain S11 Homo sapiens cDNA clone IMAGE:569379 3' similar to SW:JNK3 RAT P49187 STRESS-ACTIVATED PROTEIN KINASE JNK3 ; , mRNA sequence.
ACCESSION AA663771
VERSION   AA663771.1 GI:2617762
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 448)
AUTHORS  Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Stepcevic,M., Tan,F., Theisberg,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.
TITLE     WashU-NCI human EST Project
JOURNAL   Unpublished (1997)
COMMENT   Contact: Wilson RK
          Washington University School of Medicine
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: est@watson.wustl.edu
          This clone is available royalty-free through LMLT; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
          Possible reversed clone: similarity on wrong strand
          Seq primer: -40m13 fwd. ET from Amersham
          High quality sequence stop: 350.
          Location/Qualifiers
            1..448
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:569379"
               /sex="male"
               /tissue_type="schizophrenic brain S-11 frontal lobe"
               /dev_stage="34 years old"
               /lab_host="SOLR (kanamycin resistant)"
               /clone_id="StrataGene schizo brain S11"
               /note="Vector: Bluescript SK-; Site 1: EcoRI; Library constructed from S-11 frontal lobe, male, 34 years old, 50% caucasian, 50% Aleutian. Schizophrenic suicide. Random primed into EcoRI site of ZAP II Vector. Mass excised. Custom library. Avg insert length 1.4kb. Material obtained by Johnston N., Torrey, E.F., Yolken R., and the Stanley Neuropathology Consortium - Analysis of RNAs from the Brains of Individuals with Psychiatric Diseases (Unpublished) Stanley Neurovirology Laboratory, Johns Hopkins School of Medicine, Baltimore MD."

ORIGIN
Query Match      10.3%; Score 82.8; DB 1; Length 448;
Best Local Similarity .97.7%; Pred. No. 2.9e-08;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      626 GTACCTGAAGAGAGGCTGCTCTTACTACTACACCATTTTACTTTCTTCGAAATTC 685
|-----|
Db      210 GCACCTGAAGAGAGGCTGCTCTTACTACTACACCATTTTACTTTCTTCGAAATTC 269
|-----|
Qy      686 ATTACTCTCTGTAGATAGTTCTGT 711
|-----|

```

```

Db      270 ATTACTCTCTGTAGATAGTTCTTT 295
|-----|

RESULT 8
LOCUS   BM704479/c
DEFINITION UI-E-CK1-agb-1-15-0-UI.r1 UI-E-CK1 Homo sapiens cDNA clone
ACCESSION BM704479
VERSION   BM704479.1 GI:19017737
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 512)
AUTHORS  Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE     Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL   Genome Res. 6 (9), 791-806 (1996)
COMMENT   Contact: Soares, MB
          Coordinated Laboratory for Computational Genomics
          University of Iowa
          375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
          Tel: 319 335 8250
          Fax: 319 335 9565
          Email: bento-soares@uiowa.edu
          Tissue Procurement: Dr. Gregg Hageman
          CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
          CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
          DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
          Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
          Seq primer: M13 Reverse.
          Location/Qualifiers
            1..512
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="UI-E-CK1-agb-1-15-0-UI"
               /tissue_type="Retina Foveal and Macular"
               /dev_stage="adult"
               /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
               /clone_id="UI-E-CK1"
               /note="Organ: eye; Vector: pRTT3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-CK1 is a normalized cDNA library containing the following tissue(s): Retina Foveal and Macular. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GRCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

ORIGIN
Query Match      10.3%; Score 82.8; DB 3; Length 512;
Best Local Similarity .97.7%; Pred. No. 2.9e-08;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      626 GTACCTGAAGAGAGGCTGCTCTTACTACTACACCATTTTACTTTCTTCGAAATTC 685
|-----|
Db      413 GCACCTGAAGAGAGGCTGCTCTTACTACTACACCATTTTACTTTCTTCGAAATTC 354
|-----|

```

Qy 686 ATTACTTCCTGTAGATAGTTCTGT 711
 Db 353 ATTACTTCCTGTAGATAGTTCTTT 328

RESULT 9
 BM508552/c
 LOCUS
 DEFINITION BM508552 595 bp mRNA linear EST 12-MAR-2002
 1137A11.Y1 Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 Mus
 musculus cDNA IMAGE:5943836 5' similar to SW:MK10_HUMAN
 P53779 MITOGEN-ACTIVATED PROTEIN KINASE 10 ; mRNA sequence.
 BM508552
 VERSION BM508552.1 GI:18679695
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murine; Mus.

REFERENCE
 AUTHORS
 1 (bases 1 to 595)
 Melton, D., Brown, J., Keny, G., Permutt, A., Lee, C., Kaestner, K.,
 Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, D., Blistein, A.,
 Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
 Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, R.,
 Williams, T., Jackson, Y. and Bowers, Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Other ESTs: 1137A11.x1
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center for information on
 obtaining a clone please contact: Juliana Brown
 (brown@fas.harvard.edu)
 MGI:2006708 This sequence now available from the IMAGE consortium,
 for clone orders contact: info@image.llnl.gov
 Seq primer: -40RP from Gibco
 High quality sequence stop: 430.
 Location/Qualifiers
 1..595
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="ICR"
 /db_xref="taxon:10090"
 /clone="IMAGE:5943836"
 /sex="Both for embryonic & newborn, male for adult and
 adult islet"
 /dev_stage="Embryonic day 10.5, E12.5, E16.5, newborn,
 adult, mixed"
 /lab_host="DH10B"
 /clone_id="Melton Normalized Mixed Mouse Pancreas 1
 N1-MMS1"
 /note="Vector: DSPORT1, Site 1: Not I; Site 2: Sal I; Five
 libraries representing E10.5/12.5 pancreatic bud, E16.5
 pancreas, newborn pancreas, adult pancreas, and adult
 islets of Langerhans were separately constructed using
 Superscript Plasmid Library Kit (Life Technologies). cDNA
 was made by oligo-dT priming and size-selected by column
 fractionation. Libraries were amplified once on solid
 support and plasmid DNA from each library was prepared
 and mixed in equal amounts. The mixed library DNA was
 normalized by method #4 from Bionardo, Lennon, and Soares
 1996 Genome Research 6:791-806; 0.5 microgram
 single-stranded mixed library plasmid DNA was mixed with
 5 micrograms PCR product representing mixed library
 inserts and hybridized to an EcoT of 6. Single-stranded

ORIGIN
 (unhybridized) plasmids were isolated by hydroxyapatite
 chromatography and used to make this library."

Query Match 10.3%; Score 82.8; DB 2; Length 595;
 Best Local Similarity 97.7%; Pred. No. 3e-08;
 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 626 GTACCTGAGAGAGAGCGTCTCTTTACTACACATTTTACTCTTTCTTGAATTC 685
 Db 471 GCACCTGAGAGAGAGAGCGTCTCTTTACTACACATTTTACTCTTTCTTGAATTC 412

Qy 686 ATTACTTCCTGTAGATAGTTCTGT 711
 Db 411 ATTACTTCCTGTAGATAGTTCTTT 386

RESULT 10
 CK825957
 LOCUS
 DEFINITION CK825957 605 bp mRNA linear EST 11-MAR-2004
 1K36F03.Y5 HR85 islet Homo sapiens cDNA clone IMAGE:5783165 5'
 similar to SW:MK10_HUMAN P53779 MITOGEN-ACTIVATED PROTEIN KINASE 10
 ; mRNA sequence.
 CK825957
 VERSION CK825957.1 GI:44842882
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE
 AUTHORS
 1 (bases 1 to 605)
 Melton, D., Meadows, A., Clifton, S., Hillier, L., Marra, M., Pape, D.,
 Wylie, T., Martin, J., Blistein, A., Schmitt, A., Theising, B.,
 Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M.,
 McCann, R., Cole, R., Tsagaris, R., Williams, T., Jackson, Y. and
 Bowers, Y.
 Washu-Harvard Pancreas EST Project
 Unpublished (2000)
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 This read is a 5' RESEQUENCE of a previously sequenced pancreas
 clone
 Good hit to opposite strand read. . . wrong orientation BUT PASSED FOR
 MOUSE-PANCREAS VERIFICATION
 Possible reversed clone: similarity on wrong strand
 Seq primer: -40UP from Gibco
 High quality sequence stop: 570.
 Location/Qualifiers
 1..605
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5783165"
 /tissue_type="Purified pancreatic islet"
 /lab_host="DH10B"
 /clone_id="HR85 islet"
 /note="Organ: Pancreas; Vector: pBluescript SK(-); Site 1:
 NotI; Site 2: XhoI; cDNA made by oligo-dT priming.
 Size-selected on agarose gel. Average insert size
 XhoI site was destroyed after directional cloning.
 Amplified once. Contact information: Hiroshi Inoue, MD,
 Metabolism Div. (Alan Permutt lab), Washington University
 School of Medicine, Box 8127, 660 South Euclid Ave., St.
 Louis, MO 63110, E-mail: hinoue@image.wustl.edu, Tel:
 314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 10.3%; Score 82.8; DB 5; Length 605;
 Best Local Similarity 97.7%; Pred. No. 3e-08;
 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGCTGCTCTTTACTACACATTTCCTTTCTTCGAAATTC 685
 DB 323 GCACCTGAAGAGAGAGCTGCTCTTTACTACACATTTCCTTTCTTCGAAATTC 382
 QY 686 ATTACTCTCTGTAGATAGTTCGT 711
 DB 383 ATTACTCTCTGTAGATAGTTCGT 408

RESULT 11
 LOCUS BQ287873 618 bp mRNA linear EST 14-MAY-2002
 DEFINITION IK36f03.x1 HR85 islet Homo sapiens cDNA clone IMAGE:5783165 3', similar to SW:MK10_HUMAN P53779 MITOGEN-ACTIVATED PROTEIN KINASE 10 /, mRNA sequence.

ACCESSION BQ287873.1 GI:20658904
 VERSION BQ287873
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo
 1 (bases 1 to 618)
 Melton, D., Brown, J., Keny, G., Permut, A., Lee, C., Kaestner, K., Lamlshka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J., Cordenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaratshvili, R., Williams, T., Jackson, Y., and Bowers, Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept. of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@iobp.harvard.edu

LIBRARY was constructed by Dr. Hiroshi Inoue DNA sequencing by:
 Washington University Genome Sequencing Center for information on
 obtaining a clone please contact: Dr. Hiroshi Inoue
 (hinoue@im.wustl.edu)
 Seq primer: -40UP from Gibco
 High quality sequence stop: 369.

FEATURES
 Location/Qualifiers

1..618
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5783165"
 /cissue_type="Purified pancreatic islet"
 /lab_host="HR85 islet"
 /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact Information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permut Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 10.3%; Score 82.8; DB 3; Length 618;
 Best Local Similarity 97.7%; Pred. No. 3e-08;

Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGCTGCTCTTTACTACACATTTCCTTTCTTCGAAATTC 685
 DB 312 GCACCTGAAGAGAGAGCTGCTCTTTACTACACATTTCCTTTCTTCGAAATTC 371
 QY 686 ATTACTCTCTGTAGATAGTTCGT 711
 DB 372 ATTACTCTCTGTAGATAGTTCGT 397

RESULT 12
 LOCUS DR762335/c 921 bp mRNA linear EST 21-JUL-2005
 DEFINITION HESC4_139 B07_g1_A037 NIH_MGC_262 Homo sapiens cDNA clone IMAGE:7971903 5', mRNA sequence.

ACCESSION DR762335
 VERSION DR762335
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo
 1 (bases 1 to 921)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cga@bld-3@mail.nih.gov

CDNA Library Preparation: Express Genomics, Inc.
 Tissue Procurement: BresaGen, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 DNA Sequencing by: Laboratory for Genomics and Bioinformatics, University of Georgia
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
 plate: L1AM 17089 row: d column: 13
 Seq primer: JENREV (CAGGAACAGCATGACC)
 High quality sequence stop: 921.

FEATURES
 Location/Qualifiers

1..921
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:7971903"
 /sex="male"
 /cissue_type="embryonic stem"
 /cell_line="human embryonic stem cells"
 /lab_host="DH10B-T1 phage-resistant E. coli"
 /clone_1ib="NIH_MGC_262"
 /note="Vector: pEXpress-1; Site_1: NotI; Site_2: EcoRV; RNA obtained from human embryonic stem cells isolated from the inner cell mass of blastocyst stage embryos and differentiated to an early neural progenitor cell type. Cell line id and NIH Registry designation is BGO1. Positive for Nestin and Musashi expression. Passage number 18. cDNA primed using oligo-dT primer: 5'-pACTAGTCTAGATCGCAGCGCCGCC(1)25-3' and cloned into the EcoRV/NotI sites of pEXpress-1. This primary library is non-normalized (normalized primary library is NIH MGC 259). It was constructed by Express Genomics (Frederick, MD). Sequence ends have been trimmed to exclude vector and regions below phred quality 16. Note: this is a Mammalian Gene Collection library."

ORIGIN

Query Match 10.3%; Score 82.8; DB 10; Length 921;

KEYWORDS	EST.
SOURCE	Hom. sapiens (human)
ORGANISM	Hom. sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
AUTHORS	1 (bases 1 to 315) Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cairn, S., Leventhal, C., Thornton, M., Ramchandran, R., Whittington, J., Lerner, L., Costanzo, P., McElligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Kilia, A., Hess, J., Cochran, K., Lo, K., Ofendischer, J., Danzig, J., and Ducar, M.
TITLE	Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL	Nat. Biotechnol. 19 (5), 440-445 (2001)
PUBMED	11329013
COMMENT	Contact: Scott J. Cain Athersys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scain@athersys.com High quality sequence scop: 265. Location/Qualifiers
FEATURES	1..315 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /cell_line="HT1080" /clone_id="Athersys RAGE library" /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
ORIGIN	
Query Match	10.1%; Score 80.4; DB 2; Length 315;
Best Local Similarity	98.8%; Pred. No. 1e-07;
Matches	81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	630 CTGAAGGGAAGGCGTCCTTTACTACACATTTTGTCTTCTCTGAATTCATTA 689
Db	142 CTGAAGGGAAGGCGTCCTTTACTACACATTTTGTCTTCTCTGAATTCATTA 83
OY	690 CTCCTTGTAGTATGTTCTGT 711
Db	82 CTCCTTGTAGTATGTTCTTT 61
RESULT 16	
LOCUS	BF858136
DEFINITION	OV1-PT0202-131100-470-c12 PT0202 Homo sapiens cDNA, mRNA sequence.
VERSION	BF858136
KEYWORDS	EST.
SOURCE	EST.
ORGANISM	Hom. sapiens (human)
REFERENCE	Hom. sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
TITLE	1 (bases 1 to 386)
JOURNAL	Dies Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britonas, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P., Goldman, G.H., Carvalho, A.F., Mateuskuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.U. and Simpson, A.J.
PUBMED	11329013
COMMENT	Contact: Scott J. Cain Athersys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scain@athersys.com High quality sequence scop: 265. Location/Qualifiers
FEATURES	1..315 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /cell_line="HT1080" /clone_id="Athersys RAGE library" /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
ORIGIN	
Query Match	10.1%; Score 80.4; DB 2; Length 315;
Best Local Similarity	98.8%; Pred. No. 1e-07;
Matches	81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	630 CTGAAGGGAAGGCGTCCTTTACTACACATTTTGTCTTCTCTGAATTCATTA 689
Db	142 CTGAAGGGAAGGCGTCCTTTACTACACATTTTGTCTTCTCTGAATTCATTA 83
OY	690 CTCCTTGTAGTATGTTCTGT 711
Db	82 CTCCTTGTAGTATGTTCTTT 61
RESULT 16	
LOCUS	BF858136
DEFINITION	OV1-PT0202-131100-470-c12 PT0202 Homo sapiens cDNA, mRNA sequence.
VERSION	BF858136
KEYWORDS	EST.
SOURCE	EST.
ORGANISM	Hom. sapiens (human)
REFERENCE	Hom. sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
TITLE	1 (bases 1 to 386)
JOURNAL	Dies Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britonas, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P., Goldman, G.H., Carvalho, A.F., Mateuskuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.U. and Simpson, A.J.
PUBMED	11329013
COMMENT	Contact: Scott J. Cain Athersys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scain@athersys.com High quality sequence scop: 265. Location/Qualifiers
FEATURES	1..315 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /cell_line="HT1080" /clone_id="Athersys RAGE library" /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
ORIGIN	
Query Match	10.1%; Score 80.4; DB 2; Length 315;
Best Local Similarity	98.8%; Pred. No. 1e-07;
Matches	81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	630 CTGAAGGGAAGGCGTCCTTTACTACACATTTTGTCTTCTCTGAATTCATTA 689
Db	142 CTGAAGGGAAGGCGTCCTTTACTACACATTTTGTCTTCTCTGAATTCATTA 83
OY	690 CTCCTTGTAGTATGTTCTGT 711
Db	82 CTCCTTGTAGTATGTTCTTT 61
RESULT 16	
LOCUS	BF858136
DEFINITION	OV1-PT0202-131100-470-c12 PT0202 Homo sapiens cDNA, mRNA sequence.
VERSION	BF858136
KEYWORDS	EST.
SOURCE	EST.
ORGANISM	Hom. sapiens (human)
REFERENCE	Hom. sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
TITLE	1 (bases 1 to 386)
JOURNAL	Dies Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britonas, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P., Goldman, G.H., Carvalho, A.F., Mateuskuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.U. and Simpson, A.J.
PUBMED	11329013
COMMENT	Contact: Scott J. Cain Athersys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scain@athersys.com High quality sequence scop: 265. Location/Qualifiers
FEATURES	1..315 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /cell_line="HT1080" /clone_id="Athersys RAGE library" /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
ORIGIN	
Query Match	10.1%; Score 80.4; DB 2; Length 315;
Best Local Similarity</	

PubMed
 COMMENT
 00737800
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?li=QV1lct2-QV1-FT0202-131100-470-c12&t3=2000-11-13&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 386.
 Location/Qualifiers
 1..386
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="FT0202"
 /note="Organ: prostate tumor; Vector: puc18; Site_1: Sma1;
 Site_2: Sma1; A mini-library was made by cloning products
 derived from ORBSTS PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 ORIGIN
 Query Match 10.1%; Score 80.4; DB 2; Length 386;
 Best Local Similarity 98.8%; Pred. No. 1e-07; Indels 0; Gaps 0;
 Matches 81; Conservative 0; Mismatches 1;
 Oy 630 CTGAAGAAGAAGGCTGCTTTACTACACACATTTTACTTTCTTGATTCATTA 689
 |||||
 Db 114 CTGAAGAAGAAGGCTGCTTTACTACACACATTTTACTTTCTTGATTCATTA 55
 |||||
 Oy 690 CTTCCTGTAGATAGTTCTGT 711
 |||||
 Db 54 CTTCCTGTAGATAGTTCTTT 33
 |||||
 RESULT 17
 CBO69160 457 bp mRNA linear EST 21-JAN-2003
 i613g01.x1 HR85 islet Homo sapiens CDNA clone IMAGE:6364968 3'
 similar to SW:MK10_HUMAN P53779 MIOGEN-ACTIVATED PROTEIN KINASE 10
 ; mRNA sequence.
 ACCESSION CBO69160
 VERSION CBO69160.1 GI:27813680
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 457)
 Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
 Lemishka,I., Scazce,M., Brestelli,J., Gadowohl,G., Clifton,S.,
 Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Bliststein,A.,
 Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
 Cardenas,M., Giddons,M., McCann,R., Cole,R., Tsagarainshvili,R.,
 Williams,T., Jackson,Y. and Bowers,Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept. of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812

Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40RP from Gldco
High quality sequence stop: 369.
Location/Qualifiers
1. .457
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="6364958"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_id="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); site_1:
NotI; site_2: XhoI; cDNA made by oligo-dT priming. Size:
Size selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permut Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN
Query Match 10.1%; Score 80.4; DB 4; Length 457;
Best Local Similarity 98.8%; Pred. No. 1e-07;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTCTTTCTTGAATTCATTA 669
DB 313 CTGAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTCTTTCTTGAATTCATTA 372

QY 690 CTTCCTTGATGATTAAGTTCTGT 711
DB 373 CTTCCTTGATGATTAAGTTCTTT 394

RESULT 18
BG194386/c 789 bp mRNA linear EST 21-APR-2001
LOCUS RST13533 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.
DEFINITION BG194386
ACCESSION BG194386
VERSION BG194386.1 GI:13716073
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 789)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozar,S.,
Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cochren,K., Lo,K.,
Offenbacher,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
11329013
JOURNAL
PUBMED
COMMENT
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 397.
Location/Qualifiers
1. .789
/organism="Homo sapiens"

FEATURES
source

/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_id="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

ORIGIN
Query Match 10.1%; Score 80.4; DB 2; Length 789;
Best Local Similarity 98.8%; Pred. No. 1.1e-07;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTCTTTCTTGAATTCATTA 689
DB 142 CTGAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTCTTTCTTGAATTCATTA 83

QY 690 CTTCCTTGATGATTAAGTTCTGT 711
DB 82 CTTCCTTGATGATTAAGTTCTTT 61

RESULT 19
BG209408/c 257 bp mRNA linear EST 21-APR-2001
LOCUS RST28923 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
DEFINITION BG209408
ACCESSION BG209408
VERSION BG209408.1 GI:13731095
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 257)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozar,S.,
Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cochren,K., Lo,K.,
Offenbacher,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
11329013
JOURNAL
PUBMED
COMMENT
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 207.
Location/Qualifiers
1. .257
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_id="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

ORIGIN
Query Match 9.8%; Score 78.8; DB 2; Length 257;
Best Local Similarity 97.6%; Pred. No. 2.3e-07;
Matches 80; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

630 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTGTGAATTCATTA 689
 |||||
 Db 147 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTGTGAATTCATTA 88
 |||||
 Oy 690 CTTCCTTTGATGATTAAGTTCTGT 711
 |||||
 Db 87 CTTCCTTTGATGATTAAGTTCTTT 66
 |||||

RESULT 20
 Cj443965/c 836 bp mRNA linear EST 06-OCT-2005

LOCUS Cj443965 macaque brain cDNA library QcCE Macaca fascicularis cDNA
 DEFINITION clone QcCE-21545 5', mRNA sequence.

ACCESSION Cj443965
 VERSION Cj443965.1 GI:77250642
 KEYWORDS EST.

SOURCE Macaca fascicularis (crab-eating macaque)
 ORGANISM Macaca fascicularis

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Cercopithecidae; Cercopithecinae; Macaca.

AUTHORS 1 (bases 1 to 836)
 Osada, N., Hida, M., Kusuda, J., Tanuma, R., Hirata, M., Terao, K.,
 Suzuki, Y., Sugano, S. and Hashimoto, K.

TITLE Macaca fascicularis cDNA database
 JOURNAL Unpublished (2005)

COMMENT Contact: Naoki Osada
 Division of Biomedical Resources
 National Institute of Biomedical Innovation

Saito-Asagi 7-6-8, Ibaraki, Osaka, 567-0085, Japan
 Tel: 81-72-641-9811
 Fax: 81-72-641-9016
 Email: nosada@nibio.go.jp

URL: <http://genbank.nibio.go.jp/gbank/>.
 Location/Qualifiers

FEATURES

Source

1. 836

/organism="Macaca fascicularis"

/mol_type="mRNA"

/db_xref="taxon:9541"

/clone="QcCE-21545"

/sex="male"

/tissue_type="cerebellum cortex"

/dev_stage="adult"

/lab_host="TOP10"

/clone_lib="macaque brain cDNA library QcCE"

/note="Vector: pME18-FU3 (Acc.No. AB009864); Site_1:
 DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand
 cDNA was primed with an oligo(dT) primer
 [ATGTGGCTTTTCTTTTCTTTT]; double-stranded cDNA was
 synthesized using specific 5' and 3' primers and amplified
 by PCR. The PCR product was digested with SfiI and size
 selection was performed to exclude fragments <1.5kb. The
 SfiI-digested PCR product was cloned into distinct DraIII
 sites of pME18-FU3. XhoI sites just outside the DraIII
 sites can be used to isolate the cDNA insert. Libraries
 were constructed by oligo-capping method."

ORIGIN

Query Match 9.8%; Score 78; DB 5; Length 836;
 Best Local Similarity 94.2%; Pred. No. 3.9e-07;
 Matches 81; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 626 GTACCTAAGAGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTGTGAATTC 685
 |||||
 Db 122 GCACCTGAAGAGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTGTGAATTC 63
 |||||

Oy 686 ATTACTCTCTGTGATGATGTTCTGT 711
 |||||
 Db 62 ATTACTCTCTGTGATGATGTTCTTT 37
 |||||

RESULT 21

CR859197/c 2693 bp mRNA linear HTC 12-NOV-2004
 LOCUS CR859197
 DEFINITION Pongo pygmaeus mRNA; cDNA DKFZp459H0638 (from clone DKFZp459H0638).
 ACCESSION CR859197
 VERSION CR859197.1 GI:55729296
 KEYWORDS HTC.

SOURCE Pongo pygmaeus (orangutan)

ORGANISM Pongo pygmaeus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Pongo.

REFERENCE 1 (bases 1 to 2693)
 Koehler, K., Beyer, A., Mewes, H.W., Weil, B., Amlid, C., Osanger, A.,
 Robo, G., Han, M. and Wiemann, S.

CONSTRM The German cDNA Consortium
 TITLE Direct Submission
 JOURNAL Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
 Neuherberg, GERMANY

COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
 sequenced by BHPZ (Biomedical Research Center at the
 Heinrich-Heine-University, Dueseldorf/Germany) within the cDNA
 sequencing consortium of the German Genome Project. This clone
 (DKFZp459H0638) is available at the RZPD Deutsches
 Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.

Please contact RZPD for ordering:
<http://www.rzpd.de/cgi-bin/products/c1.cgi?cloneid=DKFZp459H0638>
 Further information about the clone and the sequencing project is
 available at <http://mips.gsf.de/projects/cdna/>.
 Location/Qualifiers

FEATURES

Source

1. 2693

/organism="Pongo pygmaeus"

/mol_type="mRNA"

/db_xref="taxon:9600"

/clone="DKFZp459H0638"

/tissue_type="cortex"

/clone_lib="459 (synonym: pcor1). Vector pSPORT1_SfiI; host
 DH10B; sites SfiI + SfiIb"

/dev_stage="adult"

/note="mitogen-activated protein kinase 10 isoform 3 (Homo
 sapiens), differentially spliced"

1. 2693

/gene="DKFZp459H0638"

638. 1792

/gene="DKFZp459H0638"

/codon_start=1

/product="hypothetical protein"

/protein_id="CAH91384.1"

/db_xref="GI:55729297"

/translation="MSKSVNDQFVSVEVSDSTFTVLKRYONLKPISGAGQIVCAAY
 DAVLBRNVAIKLSRPFQHTAKARYRLVLMKCNHKNITSLNVPFQKTLSEFO
 DVLVVELMDNALCVITONELDHRSVYLQMLCGIKLHSGIIRHDKPSNIVK
 SCKTKILDFGLARTAGTSFMWTPIVVTYRYAPAVELIOMGKENVDIWSVGIKEM
 VHKILFPERDYIDQWKKVLEQTPCEPFMKLQPTVNVYENRKYAGLTFPKLFP
 DSIFPDSHNLKASQARDLSKMLVIDAPARISVDLQHPYINWVDPAEVAP
 PQIYEQDLDERHTIDEMKELIYKVMNSEKTKNVAVGQSPSPSNQVQ"

ORIGIN

Query Match 9.7%; Score 77.2; DB 6; Length 2693;
 Best Local Similarity 96.3%; Pred. No. 6.5e-07;
 Matches 79; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 630 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTGTGAATTCATTA 689
 |||||
 Db 1775 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTGTGAATTCATTA 1716
 |||||

Oy 690 CTTCCTTTGATGATGTTCTGT 711
 |||||
 Db 1715 CTTCCTTTGATGATGTTCTTT 1694
 |||||

RESULT 22
 CF408692/c

REFERENCE	1 (bases 1 to 818)
AUTHORS	Osada,N., Hida,M., Kusuda,J., Tanuma,R., Hirata,M., Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
TITLE	Macaque fascicularis cDNA database
JOURNAL	Unpublished (2005)
COMMENT	Contact: Naoki Osada Division of Biomedical Resources National Institute of Biomedical Innovation Saito-Asagi 7-6-8, Ibaraki, Osaka, 567-0085, Japan Tel.: 81-72-641-9811 Fax: 81-72-641-9016 Email: nosada@nibio.go.jp URL: http://genebank.nibio.go.jp/gbank/ Location/Qualifiers
FEATURES	
source	1. 818 /organism="Macaque fascicularis" /mol_type="mRNA" /db_xref="taxon:9541" /clone="QcSA-19671" /sex="male" /issue_type="testis" /dev_stage="adult" /lab_host="RQP10" /clone_1lb="macaque testis cDNA library Otsa" /note="Vector: pME18S-FL3 (Acc.No. AB009864); Site 1: DraIII (CACTGTGTG); Site 2: DraII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer (AGGGGCCCTTTTCTTTTTTTTTT); double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with SfiI and size selection was performed to exclude fragments <1.5kb. The SfiI-digested PCR product was cloned into distinct DraII sites of pME18S-FL3. XhoI sites just outside the DraII sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method."
ORIGIN	
Query Match	9.4%; Score 75.6; DB 5; Length 818;
Best Local Similarity	95.1%; Prid. No. 1.4e-06;
Matches	78; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	630 CTGAAGAGAAGGCTGCCTTTACTACACCATTTTAGTCCTTTCTTGCAATTCAATTA 689 611 CTGAAGAGAAGGCTGCCTTTACTACACCATTTTAGTCCTTTCTTGCAATTCAATTA 552
DJ	690 CTTCCCTGTGATPAGTTCTGT 711 551 CTTCCCTGTGATPAGTTCTTT 530
RESULT 24	
DA807178/c	568 bp mRNA linear EST 11-NOV-2005
LOCUS	DA807178 OCBF3 Homo sapiens cDNA clone OCBF3022734 5', mRNA
DEFINITION	sequence.
ACCESSION	DA807178
VERSION	DA807178.1 GI:82045913
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo. 1 (base 1 to 568) Kimura,K., Makamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamauchi,R., Yamamoto,U., Sekine,M., Tsutsumi,K., Wakeda,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushiida,N., Yonekawa,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuna,M., Murakawa,K., Ishida,S., Ishihashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S. Identification of Transcriptional Modulation: Large-scale Promoters of Human Genes
TITLE	Promoters of Human Genes

JOURNAL
PUBMED
COMMENT

Genome Res. 16 (1), 55-65 (2006).
16344560
Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.

FEATURES
source

Location/Qualifiers
1..568
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="OCB8F3022734"
/issue_type="brain"
/dev_stage="fetal"
/clone_id="OCB8F3"
/note="Vector: pME18SFL3"

ORIGIN

Query Match 9.4%; Score 75.4; DB 9; Length 568;
Best Local Similarity 98.7%; Pred. No. 1.5e-06;
Matches 76; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 635 GGAGAGGCTGCTCTTCTTACACCACTTTTACGCTTCTTCTGATTCATTCTCC 694
|||||
Db 568 GGAGAGGCTGCTCTTCTTACACCACTTTTACGCTTCTTCTGATTCATTCTCC 509
|||||
Db 508 TTGTAGATTAAGTCTTT 492
|||||

RESULT 25
BF857793

LOCUS BF857793 408 bp mRNA linear EST 16-JAN-2001
DEFINITION OY1-FT0202-071100-465-a04 FT0202 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF857793
VERSION BF857793.1 GI:12245537
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo

REFERENCE
AUTHORS

1 (bases 1 to 408)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Bionas, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordini, S., Costa, F.P.,
Goldman, G.H., Carvalho, A.F., Matukuma, A., Bata, G.S., Simpson, D.H.,
Bunster, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL

FEATURES
source

(http://www.ludwig.org.br/scripts/gethtml2.pl?c1=QV1&c2=QV1-FT0202-
071100-465-a04&c3=2000-11-07&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 325.
Location/Qualifiers
1..408

ORIGIN

Query Match 9.2%; Score 73.2; DB 2; Length 408;
Best Local Similarity 90.7%; Pred. No. 4.6e-06;
Matches 78; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 626 GTACCTGAGAGAGAGGCTGCTCTTCTTACACCACTTTTACGCTTCTTCTGATTC 685
|||||
Db 308 GCACCTGAGAGAGAGGCTGCTCTTCTTACACCACTTTTACGCTTCTTCTGATTC 367
|||||
OY 686 ATTACTTCTTCTGATTAAGTCTGT 711
|||||
Db 368 ATTACTTCTTCTGATTAAGTCTTT 393
|||||

RESULT 26
AW314598/c

LOCUS AW314598 423 bp mRNA linear EST 25-APR-2001
DEFINITION 10855 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION AW314598
VERSION AW314598.1 GI:6743854
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.

REFERENCE
AUTHORS

1 (bases 1 to 423)
Smith, T.P.L., Grose, W.M., Preking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, V., Cho, J., Fahrnenkung, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Perera, G., Holt, I., Karayancheva, S., Liang, F.,
Quackenbush, J. and Keefe, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
PUBMED 11282978
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options.
FOR PRIMERS
FORWARD: AGGAACACCTATGACCAT
BACKWARD: GTTTCACGTCACGACG
Plate: 9 row: D column: 1
Seq primer: ATTAGTGACACTAG.

FEATURES
source

1..423
/organism="Bos taurus"
/mol_type="mRNA"

KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 551)
Smith, T.P.L., Gosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Benneit, G.L., Heaton, M.P., Laegreid, W.W., Kohrer, G.A., Chitko-McKown, C.G., Perte, G., Holt, I., Karaycheva, S., Liang, F., Quackenbush, J. and Keefe, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)

TITLE
JOURNAL PubMed 11282978
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smt@meat.mars.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.
PCR primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCACGATCAGCAGC
Plate: 46 row: M column: 8
Seq primer: ATTACGTCACCTATAG.
Location/Qualifiers
1. 551
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 280V"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

ORIGIN
Query Match 8.7%; Score 69.6; DB 7; Length 551;
Best Local Similarity 89.3%; Pred. No. 3.2e-05;
Matches 75; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGGCTGCTCTTACTACACCATTTTGTCTTCTGGAATTC 685
DB 85 GCACCTGAAGAGAGAGGCTGCTCTTCTTCAACAGCATTCTTCTTCTCGAGTTC 26

QY 686 ATTACTCTCTTGATAGTTCCT 709
DB 25 ATTACTCTCTTATAGTATGTTCT 2

RESULT 30
DV915617/c 916 bp mRNA linear EST 01-DEC-2005
LOCUS LB0288.CR_F16 GC_BGC-28 Bos taurus cDNA clone IMAGE:8222610, mRNA
DEFINITION sequence.
DV915617
VERSION DV915617.1 GI:82971369
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 916)
Moore, S., Alexander, L., Brownstein, M., Guan, L., Lobo, S., Meng, Y., Tanaguchi, M., Wang, Z., Yu, J., Prange, C., Schreiber, K., Shenmen, C.,

TITLE
JOURNAL Unpublished (2005)
COMMENT Contact: Robert Kirkpatrick
Canada's Michael Smith Genome Sciences Centre
BC Cancer Agency
Suite 100, 570 West 7th Avenue, Vancouver, British Columbia, Canada, V5Z 4S6
Tel: 1-604-707-5900 x5406
Fax: 1-604-876-3561
Email: robert@bcgsc.ca
Insert Length: 916 Std Error: 0.00
Plate: LB0288 row: F column: 16
High quality sequence stop: 916.
Location/Qualifiers
1. 916
/organism="Bos taurus"
/mol_type="mRNA"
/strain="U1 Hereford"
/db_xref="taxon:9913"
/clone="IMAGE:8222610"
/sex="female"
/tissue_type="Cerebral cortex"
/dev_stage="8.5 months old calf"
/lab_host="E. coli DH10B TI Phage resistant"
/clone_lib="GC_BGC-28"
/note="Organ: Cerebral cortex; Vector: pEXpress 1; Site 1: Blunt (5' end of cDNA); Site 2: NotI (3' end of cDNA)";

ORIGIN
Query Match 8.6%; Score 69; DB 10; Length 916;
Best Local Similarity 87.2%; Pred. No. 4.6e-05;
Matches 75; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGGCTGCTCTTACTACACCATTTTGTCTTCTGGAATTC 685
DB 813 GCACCTGAAGAGAGAGGCTGCTCTTCTTCAACAGCATTCTTCTTCTCGAGTTC 754

QY 686 ATTACTCTCTTGATAGTTCCTGT 711
DB 753 ATTACTCTCTTATAGTATGTTCTTT 728

RESULT 31
DV915213/c 801 bp mRNA linear EST 01-DEC-2005
LOCUS LB0287.CR_A06 GC_BGC-28 Bos taurus cDNA clone IMAGE:8222096, mRNA
DEFINITION sequence.
DV915213
VERSION DV915213.1 GI:82970965
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 801)
Moore, S., Alexander, L., Brownstein, M., Guan, L., Lobo, S., Meng, Y., Tanaguchi, M., Wang, Z., Yu, J., Prange, C., Schreiber, K., Shenmen, C., Wagner, L., Bala, M., Barbazuk, S., Barber, S., Babakaf, R., Beland, J., Chun, E., Del Rio, L., Gibson, S., Hanson, R., Kirkpatrick, R., Liu, J., Matsuo, C., Mayo, M., Santos, R.R., Scott, J., Tsai, M., Wong, D., Siddiqui, A., Holt, R., Jones, S.J. and Marra, M.A.
Bovine Genome Sequencing Program: Full-length cDNA Sequencing Unpublished (2005)
Contact: Robert Kirkpatrick
Canada's Michael Smith Genome Sciences Centre
BC Cancer Agency
Suite 100, 570 West 7th Avenue, Vancouver, British Columbia, Canada, V5Z 4S6

QY 626 GTACCTGAAGAGAGAGGCTGCTCTTACTACACCATTTTGTCTTTCTTCTGAATTC 685
 |||||
 Db 225 GCACCTGAAGCGAGGCTGCGCTTTTGCATCGCCATTTTGTCTTTCTTCTGAGTTC 166
 |||||

QY 686 ATTACTCTCTTGTAGATTAAGTTCTGT 711
 |||||
 Db 165 ATTACTCTCTTGTAGATTAAGTTCTTT 140
 |||||

RESULT 33
 BE652295/c 543 bp mRNA linear EST 06-SEP-2000
 LOCUS UI-M-AHO-acy-e-12-0-UI.r1 NIH BMAP MCE Mus musculus cDNA clone
 DEFINITION UI-M-AHO-acy-e-12-0-UI 5', mRNA sequence.
 ACCESSION BE652295
 VERSION BE652295.1 GI:9978138
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 543)
 Bonaldo, M.F., Lennon, G., and Soares, M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 PUBMED 8889548
 COMMENT Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9690
 Email: mestr@mail.nih.gov
 CNA Library Preparation: M.B. Soares Lab Clone distribution:
 Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
 should be noted that Benco Soares is generating a small number of
 additional specialized non-redundant arrays of BMAP cDNAs whose
 availability will be considered under appropriate and limited
 collaborative arrangements. The following repetitive elements were
 found in this cDNA sequence: 427-537, >(CA)nSimple_repeat
 Seq primer: M13 Reverse.
 Location/Qualifiers
 1..543
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-AHO-acy-e-12-0-UI"
 /dev_stage="27-32 days"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: p7713D-Pac1; Site 1: Not I; Site 2: Eco RI;
 The NIH BMAP MCE library is a non-normalized library
 constructed from mouse cerebellum. The tag is a string of
 5 nucleotides present between the Not I site and the
 oligo-dt track. The library was constructed as described
 by Bonaldo, Lennon and Soares, Genome Research 6:
 791-806, 1996. Tissue provided by Ms. Annie Novakovich,
 Zivic-Miller Laboratories."

ORIGIN
 Query Match 8.6%; Score 68.4; DB 7; Length 543;
 Best Local Similarity 87.2%; Pred. No. 6e-05;
 Matches 75; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGGCTGCTCTTACTACACCATTTTGTCTTTCTTCTGAATTC 685
 |||||
 Db 236 GCACCTGAAGCGAGGCTGCGCTTTTGCATCGCCATTTTGTCTTTCTTCTGAGTTC 177
 |||||

QY 686 ATTACTCTCTTGTAGATTAAGTTCTGT 711
 |||||

Db 176 ATTACTCTCTTGTAGATTAAGTTCTTT 151
 |||||

RESULT 34
 BU743848 553 bp mRNA linear EST 21-APR-2003
 LOCUS m149d11.y4 McCarey Eddy round spermatid Mus musculus cDNA clone
 DEFINITION IMAGE:6449444 5' similar to SW:MK10_HUMAN P53779 MITOGEN-ACTIVATED
 PROTEIN KINASE 10 ; , mRNA sequence.
 ACCESSION BU743848
 VERSION BU743848.1 GI:23691967
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 553)
 McCarey, J., Eddy, M., Marra, M., Hillier, L., Clifton, S., Pape, D.,
 Martin, J., Wylie, T., Dante, M., Bowers, Y., Theising, B., Gibbons, M.,
 Ritter, E., Tsagaris, R., Ronko, I., Maguire, L., Kennedy, S.,
 Bennett, J., Waterston, R., and Wilson, R.
 NIHES Mouse
 Unpublished (2002)
 CONTACT: McCarey/Eddy NIHES Mouse
 NIHES Mouse
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:2093756
 Seq primer: -40RP from Gibco
 High quality sequence stop: 419.
 Location/Qualifiers
 1..553
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CD-1"
 /db_xref="taxon:10090"
 /clone="IMAGE:6449444"
 /sex="male"
 /tissue_type="round spermatids, pooled from multiple mice"
 /dev_stage="60 day"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="McCarrey Eddy round spermatid"
 /note="Organ: testis; Vector: pBluescript SK+
 (Stratagene); Site 1: XhoI; Site 2: EcoRI; cDNA oligo
 dt-primed [5'-(GA)10-ACTAGTCGAGTTTCTTTTCTT-3'] and
 directionally cloned using 5' linkers 5'-AATTGGCAGCAG-3'
 and 5'-CTCGTGGCG-3'. Size selection of >400bp material
 gives average insert size ranging from 1-2 kb. Library was
 mass excised (from lambda-Unizap-XR) and resulting
 single-stranded phagemids were prepped and transformed
 into DH10B. Library contains 98.5% recombinants.
 References: J. Androl. 20:635-639 and Gene 25:263-269.
 Library constructed and donated by J. McCarey, Ph.D.
 (Southwest Foundation for Biomedical Research, Dept. of
 Genetics); excision done by E.M. Eddy, Ph.D. (National
 Institutes of Health, National Institute of Environmental
 Health Sciences). Original lambda-based library is
 available through ATCC, catalog #63423."

ORIGIN
 Query Match 8.6%; Score 68.4; DB 3; Length 553;
 Best Local Similarity 87.2%; Pred. No. 6e-05;
 Matches 75; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGGCTGCTCTTACTACACCATTTTGTCTTTCTTCTGAATTC 685
 |||||
 Db 152 GCACCTGAAGCGAGGCTGCGCTTTTGCATCGCCATTTTGTCTTTCTTCTGAGTTC 93
 |||||

RESULT 35	CB234404	763 bp	mRNA	linear	EST 10-FEB-2003
LOCUS	CB234404/c				
DEFINITION	AGENCOURT 11459319 NIH MGC 166 Mus musculus cDNA clone				
VERSION	CB234404				
KEYWORDS	CB234404.1 GI:28285982				
SOURCE	EST.				
ORGANISM	Mus musculus (house mouse)				
REFERENCE	Bukacinska, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	NIH-MGC http://mgi.nci.nih.gov/ .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: csgrb@nhi.nih.gov Tissue Procurement: T. Rajendra Kumar and Martin M. Matzuk cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov Plate: NDCM06 row: f column: 20 High quality sequence stop: 597. Location/Qualifiers				
FEATURES	1..763				
SOURCE	/organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="IMAGE:30247531" /lab_host="DH10B (phage-resistant)" /clone_11b="NIH MGC 166" /note="Organ: brain; Vector: pDNR-LIB, site 1: SfiI (ggccatcgcc); Site 2: SfiI (ggccgcctggcc); Non-normalized full-length enriched library 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCGCAGCATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 2.05 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Corp. "				
ORIGIN					
Query Match	8.6%; Score 68.4; DB 4; Length 763;				
Best Local Similarity	87.2%; Pred. No. 6.2e-05;				
Matches	75; Conservative 0; Mismatches 11; Indels 0; Gaps 0;				
OY	626 GTACCTGAGAGAGAGGCTGTCCTTTTACACACCATTTTATGCTTTCTTCTGAAATC 685				
Db	176 GCACCTGAGAGCGAGGCGCTGCGCTTGCACACGACATCTTATGCTTCTTCTGAGATC 117				
OY	686 ATTACTTCTCTGTAGATTAAGTTCTGT 711				
Db	116 ATTACTTCTCTGTAGATTAAGTTCTTT 91				
RESULT 36	AK042368	2343 bp	mRNA	linear	HTC 02-SEP-2005
LOCUS	AK042368/c				
DEFINITION	Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone: A630085G12 product: mtomgen activated protein kinase				

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
AK042368		10, full insert sequence.		
AK042368	1	GI:26335078		
HTC; CAP trapper.				
Mus musculus				
Mus musculus				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;				
Sciurognathi; Muridae; Muridae; Murinae; Mus.				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
PUBMED				
REFERENCE				
AUTHORS				
1				
Garninci, P. and Hayashizaki, Y.				
High-efficiency full-length cDNA cloning				
Meeth. Enzymol. 303, 19-44 (1999)				
10349636				
2				
Garninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,				
Itch, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
Normalization and subtraction of cap-trapper-selected cDNAs to				
prepare full-length cDNA libraries for rapid discovery of new genes				
Genome Res. 10 (10), 1617-1630 (2000)				
11042159				
3				
Shibata, K., Itch, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,				
Komoto, H., Akiyama, J., Nishi, K., Kitanai, T., Tashiro, H., Itch, M.,				
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,				
Yamamoto, R., Matsumoto, H., Sakauchi, S., Ikegami, T., Kashiwagi, K.,				
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,				
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuda, S., Kawai, J.,				
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
RIKEN integrated sequence analysis (RISA) system-384-format				
sequencing pipeline with 384 multicapillary sequencer				
Genome Res. 10 (11), 1757-1771 (2000)				
11076861				
4				
The RIKEN Genome Exploration Research Group Phase II Team and the				
FANTOM Consortium.				
Functional annotation of a full-length mouse cDNA collection				
Nature 409, 685-690 (2001)				
5				
The FANTOM Consortium, the RIKEN Genome Exploration Research Group				
Phase I and II Team.				
Analysis of the mouse transcriptome based on functional annotation				
of 60,770 full-length cDNAs				
Nature 420, 563-573 (2002)				
6				
RIKEN Genome Exploration Research Group, Genome Science Group				
(Genome Network Core Team) and the FANTOM Consortium.				
Antisense Transcription in the Mammalian Transcriptome				
Science 309, 1564-1566 (2005)				
7				
The FANTOM Consortium, Riken Genome Exploration Research Group and				
Genome Science Group (Genome Network Project Core Group).				
The transcriptional landscape of the mammalian genome				
Science 309, 1559-1563 (2005)				
8 (bases 1 to 2343)				
Adachi, J., Aizawa, K., Akiyama, T., Arikawa, T., Bono, H., Carninci, P.,				
Fukuda, S., Furuno, M., Hamaguchi, T., Hara, A., Hashizume, W.,				
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,				
Horii, F., Imotani, K., Ishii, Y., Itch, M., Kagawa, I., Kasukawa, T.,				
Kato, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,				
Koyu, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,				
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohashi, N.,				
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,				
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, Y.,				
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,				
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,				
Muramatsu, M. and Hayashizaki, Y.				
Direct Submission				
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of				
Physical and Chemical Research (RIKEN), Laboratory for Genome				
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),				
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,				
Kanagawa, 230-0045, Japan [E-mail: genome-res@sc.riken.jp,				

source	1..2729 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM_DB:9630051C24" /db_xref="taxon:10090" /clone="9630051C24" /cuisine_type="cerebellum" /clone_lib="RIKEN full-length /dev_stage="16 days neonate"
misc_feature	1..2729 /note="mitogen activated protein kinase 10 [MG]MG:1346863 GB NM_009158, evidence: B1ASTN, 99%, match=21391. putative"
ORIGIN	
Query Match	8.6%; Score 68.4; DB 6; Length 2729; Best Local Similarity 87.2%; Pred. No. 6,9e-05; Matches 75; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY	626 GTACCTGAAGAGAGAGGCTGCTCTTACTACACATTTTACTGCTTCTTGATTC 685 1774 GCACCTGAAGAGAGGCTGCTCTTACTACACATTTTACTGCTTCTTGATTC 1715
DB	686 ATTACTCTCTTGATAGATTAAGTTCTGT 711 1714 ATTACTCTCTTGATAGATTAAGTTCTTT 1689
Db	
RESULT 38	
LOCUS	BF854904 561 bp mRNA linear EST 16-JAN-2001
DEFINITION	MR1-FN0210-301000-001-b10 FN0210 Homo sapiens cDNA, mRNA sequence.
ACCESSION	BF854904
VERSION	BF854904.1 GI:12242648
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 561) Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britone, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Balda, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
AUTHORS	
JOURNAL	
PUBMED	
COMMENT	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 10737800 Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR1&cl2=MR1-FN0210- 301000-001-b10&cl3=2000-10-30&cl4=1) Seq primer: puc 18 Forward High quality sequence stop: 559. Location/Qualifiers 1..561 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult"
FEATURES	
source	

ORIGIN	
Query Match	8.5%; Score 67.8; DB 2; Length 561; Best Local Similarity 95.8%; Pred. No. 8,3e-05; Matches 69; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	640 AGGCTGCTCTTACTACACACATTTTACTGCTTCTTCTGTAATCATTAATCTCTGTA 699 455 AGGCTGCTCTTACTACACACATTTTACTGCTTCTTCTGTAATCATTAATCTCTGTA 514
DB	
QY	700 GATTAAGTTCTGT 711 515 GATTAAGTTCTTT 526
Db	
RESULT 39	
LOCUS	AK163206 2629 bp mRNA linear HTC 21-SEP-2005
DEFINITION	Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730093C22 product:mitogen activated protein kinase 10, full insert sequence.
ACCESSION	AK163206
VERSION	AK163206.1 GI:74190275
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE	1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 10349636
REFERENCE	2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 11042159
REFERENCE	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsubiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 11076861
REFERENCE	4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuenli, P., Lewis, S., Matsumo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staahl, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bulic, C.,

```

Fletcher,C., Fujita,M., Gariboldi,M., Guertincich,S., Hill,D.,
Hofmann,M., Hume,D.A., Kamita,M., Lee,N.H., Lyons,P.,
Marchionni,L., Mashima,J., Marzarelli,J., Mombaerts,P., Nordone,P.,
Ring,B., Ringwald,M., Rodriguez,J., Sakamoto,N., Saeki,H.,
Sato,K., Schonbach,C., Seta,T., Shibata,Y., Storch,K.F., Suzuki,H.,
Toyo-Oka,K., Wang,K.H., Weitz,C., Whitaker,C., Wilming,L.,
Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohsaki,S.,
and Hayashizaki,Y.
RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
11217851
CONSRTM
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
5
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,T., Otsu,N., Saito,R., Suzuki,H., Yamana,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Gotohori,T., Baldarelli,R., Hill,D.P., Bult,C.,
Hume,D.A., Quackenbush,J., Schiraldi,M., Kanapin,A., Matsuda,H.,
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
Chothia,C., Corbani,L.E., Cousins,S., Della,E., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
Guertincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
Kurochkin,I.V., Lee,Y., Lennard,B., Lyons,P.A., Maglott,D.R.,
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Petosa,G., Pesole,G.,
Petrovsky,N., Pillai,R., Pontius,J.V., Qi,D., Ramachandran,S.,
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
Sandelin,A., Schneider,C., Sempke,C.A., Setou,M., Shimada,K.,
Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
Verardo,R., Wagner,L., Wahlstedt,C., Wang,Y., Watanabe,Y.,
Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Hayakawa,N., Hirozane-Kishikawa,T., Komori,K., Nakamura,M.,
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,M., Aizawa,K.,
Arakawa,T., Fukuda,S., Hara,A., Hashizume,M., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shingawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,B.S.,
Rogers,D., Birney,E. and Hayashizaki,Y.
FANTOM Consortium
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420 (6915), 563-573 (2002)
12466851
CONSRTM
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
6
Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C.,
Maeda,N., Oyama,R., Ravasi,T., Lennard,B., Wells,C., Kodzius,R.,
Shimokawa,K., Davis,V.B., Brenner,S.E., Batalov,S., Forrest,A.R.,
Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E.,
Ambesi-Impombato,A., Apweiler,R., Attalaya,R.N., Bailey,T.B.,
Banasal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M.,
Chiu,K.P., Choudhary,V., Christofels,A., Clutterbuck,D.R.,
Crome,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G.,
di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G.,
Fletcher,C.F., Fukushima,T., Furuno,M., Furuki,S., Gariboldi,M.,
Georgii-Hemming,P., Gingeras,T.R., Gotohori,T., Green,R.E.,
Guertincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N.,
Hill,D., Hummelbeck,L., Iacono,M., Ikey,K., Iwama,A., Ishikawa,T.,
Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,T.,
Kitano,H., Kollas,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K.,
Kurochkin,I.V., Lareau,L.F., Lazarovic,D., Lipovich,L., Liu,J.,
Liu,S., McMilliam,S., Madan Babu,M., Madera,M., Marchionni,L.,
Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S.,
Morris,K., Mortazavi,T., Mulder,N., Nakano,N., Nakachi,H.,
Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O.,
Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavoni,G.,
Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z.,
Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A.,
Schneider,C., Schonbach,C., Sekiguchi,K., Sempke,C.A., Seta,S.,
Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D.,
Sinciat,B., Sperling,S., Stupka,E., Sugtara,K., Sultana,R.,
Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S.,
Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R.,
Wagner,J., Weichmann,S.A., Weng,H.R., van Nimwegen,E., Verardo,R.,
Wei,C.L., Yagi,K., Yamashita,H., Zdobychsky,E., Zhu,S., Zimmer,A.,
Hilde,M., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T.,
Brusic,V., Quackenbush,J., Wahlstedt,C., Mattick,J.S., Hume,D.A.,
Kai,C., Saeki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M.,
Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imanura,K., Itoh,M.,
Kato,T., Kawaji,H., Kawasawa,Y., Kawashima,N., Kawashima,T., Kojima,M.,
Kondo,S., Kono,H., Nakano,K., Niimura,N., Nishio,T., Okada,M.,
Plessey,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K.,
Wataniki,A., Okamura-Ohno,Y., Suzuki,H., Kawai,J., Kawai,H., Hayashizaki,Y.
The transcriptional landscape of the mammalian genome
Science 309 (5740), 1559-1563 (2005)
16141072
CONSRTM
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
7
Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakashima,M.,
Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H.,
Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T.,
Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L.,
Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A.,
Chalk,A.M., Mortazavi,T., Wang,Y., Liang,Z., Lennard,B. and
Wahlstedt,C.
RIKEN Genome Exploration Research Group
Antisense transcription in the mammalian transcriptome
Science 309 (5740), 1564-1566 (2005)
16141073
CONSRTM
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
8 (bases 1 to 2629)
Arakawa,T., Carninci,P., Fukuda,S., Hashizume,M., Hayashida,K.,
Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S.,
Kawai,J., Kojima,M., Kono,M., Murata,M., Nakamura,M., Niimura,N.,
Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Saeki,D.,
Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Wataniki,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Substition
Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa, 230-0045, Japan (E-mail:genome-res@gs.c.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers
1. 2629
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:A730093C22"
/db_xref="taxon:10090"
/clone="A730093C22"
/tissue_type="cerebellum"
/clone_1ib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="7 days neonate"
518..1774
/note="unlabeled protein product; microg activated protein
kinase 10 (MGD) [MG:1346863 GB|BC046625, evidence: BLASTN,
99%, match=1759]
putative"
/codon_start=1
/protein_id="BAE37234.1"
/db_xref="GI:74190276"
/translation="MSLPLFLYCSPTLDVKIAFCQCPDKAVDSIAKHYMSKSV
DNQFISVGGSTFVLKRYONLKPISGAGCIVCAADAVLDKRVAAKKLSRPQNO
THAKAYRELIVMKCNKNIISLNVFTPKTELEPDDVYVMEIEMANILCOVOME
LDHMSYLVLYOMLCIGIKHLSAGIIRHDLKPSNIVVKSDDLKILDFGLARTAGTSF

```

ORIGIN

Query Match 8.4%; Score 67; DB 6; Length 2629;
 Best Local Similarity 83.5%; Pred. No. 0.00014;
 Matches 76; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

MTPTVTVTRRYRPAEVLIGMKYKENVDSVCGIMGEMVHRKILFREGDVIIDANKVI
 EQLGTPCEPFRKCLQPTVKNVVENRPRKAGLTPFKLPDSLFPADSEHNKLAKSQARD
 LLSKMLVIDPAKRIISVDLQHPYINWYDPAVEAPPDPIYDKQJDERBHTIEWKE
 LIYKVENNSEKTKNGVVKQSPSPA"

QY 621 AGTAGAGCTGAAGAGAGAGCTGCTCTTTTACTACACCATTTTACTCTTCTCTG 680
 |||||
 DB 1778 AGTTCAAGCTGAAGGAGGAGGCTGGCTTTGACTACGCCATCTTACTCTCTG 1719
 |||||
 QY 681 AATTCACTCTCTGTTAGATTAAGTTCTGT 711
 |||||
 DB 1718 AGTTCACTTACCCTCTGTTAGATTAAGTTCTTT 1688
 |||||

RESULT 40
 CB607972/c 576 bp mRNA linear EST 16-MAY-2003
 LOCUS
 DEFINITION AMGNNUC:NRDGI-00127-G9-A nrdg1 (10855) Rattus norvegicus cDNA clone
 nrdg1-00127-g9 5', mRNA sequence.

ACCESSION CB607972.1 GI:29547657
 VERSION
 KEYWORDS
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus

REFERENCE
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Rattus.

AUTHORS
 TITLE Amgen Rat EST Program
 JOURNAL Unpublished (2003)
 COMMENT Contact: Dan Fitzpatrick

Amgen, Inc
 One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
 Tel: 805 447-4881
 Plate: 00127 row: 9 column: 9.

FEATURES
 source
 1..576
 Location/Qualifiers

/organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /clone="nrdg1-00127-g9"
 /tissue_type="Dorsal Root Ganglia"
 /clone_lib="nrdg1 (10855)"
 /note="Vector: PSORT1; Site_1: SalI; Site_2: NotI; rat
 dorsal root ganglia"

ORIGIN

Query Match 8.3%; Score 66.8; DB 4; Length 576;
 Best Local Similarity 86.0%; Pred. No. 0.00014;
 Matches 74; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGCTGCTCTTTTACTACACCATTTTACTCTTCTCTGAAATTC 685
 |||||
 DB 438 GCACCTGAAGAGTGAAGGCTGGCTTTGACTACGCCCTTACTCTTCTCTGAGTTC 379
 |||||
 QY 686 ATTACTCTCTGTAGATTAAGTTCTGT 711
 |||||
 DB 378 ATTACTCTCTGTAGATTAAGTTCTTT 353
 |||||

RESULT 41
 CFS35846/c 570 bp mRNA linear EST 12-SEP-2003
 LOCUS
 DEFINITION UI-M-GHO-cha-a-06-0-UI.r1 NIH_BMAP_GHO Mus musculus cDNA clone
 IMAGE:3053369 5', mRNA sequence.
 ACCESSION CFS35846
 VERSION CFS35846.1 GI:34587814

KEYWORDS
 SOURCE
 ORGANISM

EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
 TITLE NIH-MGC National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
 This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)
 The following repetitive elements were found in this cDNA
 sequence: 383-493, >(CA)n#Simple_repeat
 Seq primer: pyx-5.

FEATURES
 source

Location/Qualifiers
 1..570
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30533669"
 /tissue_type="whole brain"
 /dev_stage="1, 5, and 15 days newborn"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH-BMAP_GHO"
 /note="Organ: Brain; Vector: pyx-Asc; Site 1: EcoR I;
 Site 2: Not I; The library was constructed according
 Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pyx-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is CGACTGAAAT. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemlin Chin, Ph.D.,
 program coordinator."

ORIGIN

Query Match 8.2%; Score 66; DB 5; Length 570;
 Best Local Similarity 87.8%; Pred. No. 0.00021;
 Matches 72; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 630 CTGAAGGAGAGAGCTGCTCTTTTACTACACCATTTTACTCTTCTCTGAAATCATTA 689
 |||||
 DB 183 CTGAAGGAGAGAGCTGCTTTGACTACGCCATCTTACTCTTCTCTGAGTTCAITTA 124
 |||||
 QY 690 CTTCCTGTAGATTAAGTTCTGT 711
 |||||
 DB 123 CCTCCTGTAGATTAAGTTCTTT 102
 |||||

RESULT 42
 BM944347/c 578 bp mRNA linear EST 14-MAR-2002
 LOCUS
 DEFINITION UI-M-EHOP-bvg-f-13-0-UI.r1 NIH_BMAP_EHOP Mus musculus cDNA clone
 IMAGE:5695500 5', mRNA sequence.
 ACCESSION BM944347
 VERSION BM944347.1 GI:19427932
 KEYWORDS
 SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 578)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

REFERENCE

Email: cgapbs-remail.nih.gov

AUTHORS

Tissue Procurement: Dr. James Lin, University of Iowa

TITLE

CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

JOURNAL

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

COMMENT

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

REFERENCE

Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLNL at:

TITLE

<http://image.llnl.gov>

JOURNAL

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

COMMENT

Seq primer: PYX-5.

FEATURES

Location/Qualifiers

SOURCE

1. 578

REFERENCE

/organism="Mus musculus"

AUTHORS

/mol_type="mRNA"

TITLE

/strain="C57BL/6"

JOURNAL

/db_xref="taxon:10090"

COMMENT

/clone="IMAGE:5695500"

REFERENCE

/tissue_type="whole brain"

AUTHORS

/dev_stage="embryo 18.5 dpc"

TITLE

/lab_host="DH10B (T1 phage resistant)"

JOURNAL

/clone_1lb="NIH BMAP_EH0P"

COMMENT

/note="Organ: brain; Vector: PYX-Asc; Site 1: Ecor I; Site 2: Not I; The library was constructed according to Bonafide, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with Not I, and then cloned directionally into pTX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCCAGAC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP). 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 8.2%; Score 66; DB 3; Length 578; Best Local Similarity 87.8%; Pred. No. 0.00021; Matches 72; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 630 CTGAAGGAGAGAGGCTGCTTTTACTACACCATTTTACTGCTTTCTGAAATCATTA 689
 DB 335 CTGAAGGAGAGAGGCTGCTTTTACTACACCATTTTACTGCTTTCTGAAATCATTA 276
 QY 690 CTTCCTTTAGATTAAGTTCTGT 711
 DB 275 CCTCCTTTAGATTAAGTTCTTT 254

RESULT 43

LOCUS

CX221469/c

DEFINITION

639 bp mRNA linear EST 29-DEC-2004

ACCESSION

MNS38129 Mouse Neurosphere Normalized CDNA library Mus musculus

VERSION

CX221469.1

KEYWORDS

GI:56876761

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

REFERENCE

1 (bases 1 to 639)

AUTHORS

Williams, C., Wirta, V., Lundberg, J. and Friesen, J.

TITLE

Expressed sequence tags of CDNA clones from murine neurospheres

JOURNAL

Unpublished (2005)

COMMENT

Contact: Williams, C.

REFERENCE

Institution of Biotechnology

AUTHORS

Albanova University Center, KTH-Royal Institute of Technology, 106

TITLE

91 Stockholm, Sweden

JOURNAL

Tel: +4685378332

COMMENT

Fax: +4685378481

REFERENCE

Email: cecilia.williams@biotech.kth.se

TITLE

Seq primer: MJRW

JOURNAL

Location/Qualifiers

SOURCE

1. 639

REFERENCE

/organism="Mus musculus"

AUTHORS

/mol_type="mRNA"

TITLE

/strain="C57BL/6"

JOURNAL

/db_xref="taxon:10090"

COMMENT

/sex="MALE"

REFERENCE

/tissue_type="lateral wall of lateral ventricle"

AUTHORS

/cell_type="Early passage neurosphere"

TITLE

/dev_stage="Adult"

JOURNAL

/clone_1lb="Mouse Neurosphere Normalized CDNA library"

COMMENT

/note="Organ: Adult Brain; Vector: pCMVSPORT6.0; A CDNA library was constructed in pCMVSPORT6.0 from RNA isolated from neurospheres of adult male and female mice. Custom normalized CDNA library by Invitrogen/Resgen"

ORIGIN

Query Match 8.2%; Score 66; DB 8; Length 639; Best Local Similarity 87.8%; Pred. No. 0.00022; Matches 72; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 630 CTGAAGGAGAGAGGCTGCTTTTACTACACCATTTTACTGCTTTCTGAAATCATTA 689
 DB 397 CTGAAGGAGAGAGGCTGCTTTTACTACACCATTTTACTGCTTTCTGAAATCATTA 338
 QY 690 CTTCCTTTAGATTAAGTTCTGT 711
 DB 337 CCTCCTTTAGATTAAGTTCTTT 316

RESULT 44

LOCUS

CF951683

DEFINITION

721 bp mRNA linear EST 20-NOV-2003

ACCESSION

UI-M-HLO-cmc-a-15-0-UI_r1 NIH BMAP_HLO Mus musculus cDNA clone

VERSION

CF951683

KEYWORDS

CF951683.1 GI:38467552

SOURCE

EST.

ORGANISM

Mus musculus (house mouse)

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

1 (bases 1 to 721)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

REFERENCE

Email: cgapbs-remail.nih.gov

AUTHORS

Tissue Procurement: Dr. James Lin University of Iowa

TITLE

CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

JOURNAL

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

COMMENT

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

REFERENCE

Clone Distribution: Distribution information can be found at

TITLE

<http://genome.uiowa.edu/distribution/mouse1.html>

JOURNAL

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

COMMENT

The following repetitive elements were found in this CDNA

REFERENCE

Sequence: 409-519, >(CA)nSimple_repeat


```

/organism="Rattus norvegicus"
/mol_type="mrna"
/db_xref="taxon:10116"
/clone="R8C20650"
/tissue_type="pancreatic islet"

```

```

/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="Chest780f8"
/dev_stage="16 day embryo"
/lab_host="DH10B"
/clone_id="CSBQCHN57"
/notes="Organ: brain; Vector: pBluescript II KS(+); Site:1:
EcoRI; Site:2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was bluntend, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1996) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996) : 791, except that a significantly longer
reannealing hybridization was used."

```

ORIGIN	
Query Match:	8.0% Score 64; DB 3; Length 331;
Best Local Similarity	93.1% Pred. NO. 0.00059;
Matches 67; Conservative	0; Mismatches 5; Indels 0; Gaps 0;

QY 630 CTGAGAGAGAGGCTGCTTTTACTACACCATTTTACTTTCTTCTTCTGATTCCTTA 689
 DB 72 CTGAGAGAGAGGCTGCTTTTACTACACCATTTTCTTCTTCTGAGAAATTCATTA 13
 QY 690 CTCTCTGTAGA 701
 DB 12 CTCTCTGTAGA 1

RESULT 49
 BU725204 778 bp mRNA linear EST 09-MAR-2004
 LOCUS BU725204 MF01FFA cDNA Oryzias latipes cDNA clone MF01FFA035b01 3',
 DEFINITION mRNA sequence.
 ACCESSION BU725204 GI:45266296
 VERSION BU725204.1
 KEYWORDS EST.
 SOURCE Oryzias latipes (Japanese medaka)
 ORGANISM Oryzias latipes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Perciformes; Atherinomorpha;
 Belontiiformes; Adrianchthyidae; Oryziinae; Oryzias.
 1 (bases 1 to 778)
 Kohara, Y., Shin-i, T., Kimura, T., Narita, T., Jindo, T. and Takeda, H.
 Medaka EST Project in Takeda's lab
 Unpublished (2001)
 Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.
 Location/Qualifiers
 1. 778
 /organism="Oryzias latipes"
 /mol_type="mRNA"
 /strain="Md-RR"
 /db_xref="taxon:8090"
 /clone="MF01FFA035b01"
 /sex="mixture of female and male"
 /tissue_type="whole embryo"
 /dev_stage="fry stage 40"
 /clone_id="MF01FFA cDNA"

ORIGIN
 Query Match 7.4%; Score 59; DB 2; Length 778;
 Best Local Similarity 74.7%; Pred. No. 0.0089;
 Matches 74; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 613 TCACGAGAGTGAAGTCTGAGAGAGAGGCTGCTTTTACTACACCATTTTACTCTT 672
 DB 183 TTATGACACTGAGAGTCACTGAGAGAGGCTGCTTCAACAAGCCATTCCTGCTT 242
 QY 673 TTCTTCTGAATTCATTCCTCTGTAGATTAAGTTCTGT 711
 DB 243 CTCCTCAAGTCAATGACCTCTTTGTAGATTAGTTCTTT 281

RESULT 50
 CX143962 645 bp mRNA linear EST 03-JAN-2005
 LOCUS CX143962 NCCGWA 03RT Oncorhynchus mykiss cDNA 3', mRNA sequence.
 DEFINITION 1283656 NCCGWA 03RT Oncorhynchus mykiss cDNA 3', mRNA sequence.
 ACCESSION CX143962
 VERSION CX143962.1 GI:5700617
 KEYWORDS EST.
 SOURCE Oncorhynchus mykiss (rainbow trout)
 ORGANISM Oncorhynchus mykiss
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 1 (bases 1 to 645)

REFERENCE
 1 (bases 1 to 645)

AUTHORS Rexroad, C.E., Rise, M., Koop, B., von Schalburg, K. and Yao, J.
 TITLE 03RT yb1b, NCCGWA/WVU EST Project, Phase II, in collaboration with GRASP
 JOURNAL Unpublished (2004)
 COMMENT Contact: Rexroad CE
 USDA, ARS, National Center for Cool and Cold Water Aquaculture
 11876 Leetown Road, Kearneysville, WV 25430, USA
 Tel: 304 725 0351
 Fax: 304 725 0351
 Email: crexroad@nccgwa.ars.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.
 Place: 116 row: J column: 6
 Seq primer: GTATATCGACTCATCTATAGGG.
 Location/Qualifiers
 1. 645
 /organism="Oncorhynchus mykiss"
 /mol_type="mRNA"
 /db_xref="taxon:8022"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_id="NCCGWA 03RT"
 /note="Vector: pBluescript SK+; This is a normalized (Coc
 = 5) O. mykiss whole juvenile library created by Matthew
 L. Rise from approximately 4 month old O. mykiss
 (Tzenzai-cut Lake strain) obtained from Vancouver Island
 Trout Hatchery (Duncan, B.C.)."

ORIGIN
 Query Match 7.0%; Score 55.8; DB 8; Length 645;
 Best Local Similarity 72.7%; Pred. No. 0.048;
 Matches 72; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 613 TCACGAGAGTGAAGTCTGAGAGAGAGGCTGCTTTTACTACACCATTTTACTCTT 672
 DB 201 TTATGACACTGAGAGTCACTGAGAGAGGCTGCTTCAACAAGCCATTCCTGCTT 142
 QY 673 TTCTTCTGAATTCATTCCTCTGTAGATTAAGTTCTGT 711
 DB 141 CTCCTCAAGTCAATGACCTCTTTGTAGATTAGTTCTTT 103

Search completed: July 19, 2006, 20:15:06
 Job time : 4924 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceeleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2006, 18:46:15 ; Search time 204 Seconds
(without alignments)
7337.682 Million cell updates/sec

Title: US10723681MOD.SEQ

Perfect score: 1 acatttcctaaactctta.....caataactacgtttgatg 800

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents NA:*

- 1: /EMC_Celerra_SIDS3/prodata/2/ina/1.COMB.seq:*
- 2: /EMC_Celerra_SIDS3/prodata/2/ina/5.COMB.seq:*
- 3: /EMC_Celerra_SIDS3/prodata/2/ina/6.COMB.seq:*
- 4: /EMC_Celerra_SIDS3/prodata/2/ina/6.COMB.seq:*
- 5: /EMC_Celerra_SIDS3/prodata/2/ina/7.COMB.seq:*
- 6: /EMC_Celerra_SIDS3/prodata/2/ina/7.COMB.seq:*
- 7: /EMC_Celerra_SIDS3/prodata/2/ina/7.COMB.seq:*
- 8: /EMC_Celerra_SIDS3/prodata/2/ina/7.COMB.seq:*
- 9: /EMC_Celerra_SIDS3/prodata/2/ina/7.COMB.seq:*
- 10: /EMC_Celerra_SIDS3/prodata/2/ina/7.COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	82.8	10.3	1422	3	US-09-909-650B-24
2	82.8	10.3	1505	3	US-09-130-616-178
3	82.8	10.3	1505	3	US-09-023-655-952
4	82.8	10.3	1505	3	US-09-165-522-1
5	82.8	10.3	2367	3	US-09-165-522-3
6	82.8	10.3	2677	3	US-09-566-921-34
7	80.4	10.1	1306	3	US-09-909-650B-22
8	80.4	10.1	1773	3	US-09-130-616-177
9	80.4	10.1	1773	3	US-09-165-522-4
10	80.4	10.1	2131	3	US-09-771-616A-87
11	80.4	10.1	2372	3	US-09-130-616-174
12	80.4	10.1	2372	3	US-09-016-434-1389
13	80.4	10.1	2372	3	US-09-165-522-6
14	80.4	10.1	2372	3	US-09-165-522-7
15	80.4	10.1	2982	3	US-09-566-921-33
16	66.8	8.3	1975	3	US-09-130-616-175
17	66.8	8.3	1975	3	US-09-165-522-9
18	64.4	8.1	2522	3	US-09-130-616-176
19	64.4	8.1	2522	3	US-09-165-522-11
20	55.8	7.0	48313	3	US-09-949-016-17088
21	50.8	6.3	1408	3	US-09-130-616-165
22	48.8	6.1	2372	3	US-10-104-047-1930
23	48.4	6.0	1619	3	US-09-130-616-173

24	48.4	6.0	1780	3	US-08-230-602B-17	Sequence 17, Appl
25	48.4	6.0	1780	3	US-09-861-012A-17	Sequence 17, Appl
26	48.4	6.0	1780	3	US-09-861-098A-17	Sequence 17, Appl
27	48.4	6.0	1780	3	US-09-861-097-17	Sequence 17, Appl
28	48.4	6.0	1780	7	PCT-US94-12913A-17	Sequence 17, Appl
29	48.4	6.0	1782	3	US-09-209-668-16	Sequence 169, Appl
30	48.4	6.0	1782	3	US-09-130-616-169	Sequence 1750, A
31	48.4	6.0	132456	3	US-09-949-016-13750	Sequence 171, App
32	46.8	5.8	1352	3	US-09-130-616-171	Sequence 933, App
33	46.8	5.8	1352	3	US-09-023-655-953	Sequence 5346, App
34	46.8	5.8	1352	3	US-09-949-016-5346	Sequence 172, App
35	46.8	5.8	1523	3	US-09-130-616-172	Sequence 19, Appl
36	46.8	5.8	1769	2	US-08-253-155A-19	Sequence 1377, Ap
37	46.8	5.8	1873	3	US-09-016-434-1437	Sequence 53117, A
38	46	5.8	601	3	US-09-949-016-53117	Sequence 22, Appl
39	46	5.8	1141	3	US-09-806-708B-22	Sequence 13276, A
40	46	5.8	100877	3	US-09-949-016-13276	Sequence 53116, A
41	45.6	5.7	601	3	US-09-949-016-53116	Sequence 2813, Ap
42	44.6	5.6	1349	3	US-09-621-976-2813	Sequence 168, App
43	44.4	5.5	1365	3	US-09-130-616-168	Sequence 166, App
44	44.4	5.5	1365	3	US-09-130-616-166	Sequence 1139, App
45	44.4	5.5	1365	3	US-09-016-434-1139	Sequence 2813, Ap
46	42.4	5.3	832	3	US-09-621-976-2813	Sequence 167, App
47	42.4	5.3	1311	3	US-09-130-616-167	Sequence 14, Appl
48	42	5.2	1418	3	US-09-209-668-14	Sequence 164, App
49	42	5.2	1418	3	US-09-130-616-164	Sequence 11, Appl
50	42	5.2	1418	3	US-08-220-602B-11	Sequence 11, Appl
51	42	5.2	1418	3	US-09-861-012A-11	Sequence 11, Appl
52	42	5.2	1418	3	US-09-861-098A-11	Sequence 11, Appl
53	42	5.2	1418	3	US-09-861-097-11	Sequence 11, Appl
54	42	5.2	1418	7	PCT-US94-12913A-11	Sequence 11, Appl
55	42	5.2	1514	3	US-09-949-016-2008	Sequence 208, Ap
56	42	5.2	1893	3	US-09-417-197-62	Sequence 62, Appl
57	42	5.2	1902	3	US-09-949-016-15509	Sequence 44, Appl
58	42	5.1	640681	3	US-09-417-197-44	Sequence 1, Appl
59	41	5.1	1908	3	US-08-945-558-50	Sequence 50, Appl
60	40.8	5.1	1908	3	US-08-945-558-50	Sequence 50, Appl
61	40.8	5.1	1908	3	US-09-528-784A-4	Sequence 50, Appl
62	40.8	5.1	1908	3	US-09-528-784A-50	Sequence 50, Appl
63	40.8	5.1	1908	3	US-09-569-098A-26	Sequence 50, Appl
64	40.8	5.1	1908	3	US-09-569-098A-50	Sequence 4, Appl
65	40.8	5.1	1908	3	US-08-945-558-4	Sequence 4, Appl
66	40.8	5.1	1991	3	US-08-990-571-4	Sequence 4, Appl
67	40.8	5.1	1991	3	US-08-723-142A-4	Sequence 4, Appl
68	40.8	5.1	1991	3	US-09-528-784A-4	Sequence 4, Appl
69	40.8	5.1	1991	3	US-09-569-098A-4	Sequence 4, Appl
70	40.8	5.1	50000	3	US-09-662-254B-26	Sequence 26, Appl
71	40.8	5.1	134987	3	US-09-949-016-15348	Sequence 15348, A
72	40.8	5.1	134987	3	US-09-949-016-15348	Sequence 15348, A
73	40.8	5.1	134987	3	US-09-949-016-15348	Sequence 15350, A
74	40.8	5.1	134987	3	US-09-949-016-15507	Sequence 15507, A
75	40.8	5.1	134987	3	US-09-949-016-15508	Sequence 15508, A
76	40.8	5.1	134987	3	US-09-949-016-15509	Sequence 15509, A
77	40.6	5.1	105679	3	US-09-949-016-12360	Sequence 12360, A
78	40.4	5.0	1582	3	US-08-545-196B-10	Sequence 10, Appl
79	40.4	5.0	1582	3	US-08-545-196B-12	Sequence 12, Appl
80	40.4	5.0	1582	5	US-09-109-082A-10	Sequence 10, Appl
81	40.4	5.0	1582	5	US-09-109-082A-12	Sequence 12, Appl
82	40.4	5.0	238815	3	US-09-949-016-16774	Sequence 16774, A
83	40	5.0	260286	3	US-09-949-016-17037	Sequence 17037, A
84	40	5.0	260286	3	US-09-949-016-12106	Sequence 12106, A
85	40	5.0	786431	3	US-09-751-389-3	Sequence 3, Appl
86	39.6	5.0	3355	3	US-09-120-988-5	Sequence 5, Appl
87	39.6	5.0	3355	3	US-09-662-254B-62	Sequence 62, Appl
88	39.4	4.9	1452	3	US-09-248-796A-3739	Sequence 3739, Ap
89	39.4	4.9	1452	3	US-09-949-016-14584	Sequence 14584, A
90	39.2	4.9	601	3	US-09-949-016-15830	Sequence 15830, A
91	39.2	4.9	175265	3	US-09-949-016-15830	Sequence 2679, Ap
92	39.2	4.9	192506	3	US-09-328-352-2679	Sequence 15830, A
93	38.8	4.8	991	3	US-09-790-988-1	Sequence 1, Appl
94	38.8	4.8	640681	3	US-09-949-016-68185	Sequence 68185, A
95	38.4	4.8	601	3	US-09-949-016-68185	Sequence 173, App
96	38.4	4.8	1755	3	US-09-248-796A-3448	Sequence 3448, Ap

C 97 38.4 4.8 32392 3 US-09-662-254B-27 Sequence 27, Appl
C 98 38.4 4.8 156324 3 US-09-949-016-13749 Sequence 13749, A
C 99 38 4.8 601 3 US-09-949-016-68481 Sequence 68481, A
C 100 38 4.8 130724 3 US-09-949-016-13753 Sequence 13753, A

ALIGNMENTS

RESULT 1

US-09-909-650B-24/c
Sequence 24, Application US/09090650B
Patent No. 6649388
GENERAL INFORMATION:
APPLICANT: Aventis Pharmaceuticals Inc.
APPLICANT: Fournier, Alain
APPLICANT: Maury, Isabelle
APPLICANT: Zhou-Liu, Qing
APPLICANT: Desanlis-Cremont, Francine
TITLE OF INVENTION: Polypeptides Derived From JNK3
FILE REFERENCE: ST99003-US-CNT-1
CURRENT APPLICATION NUMBER: US/09/909,650B
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: PCT/FR00/00104
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/122,175
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: US 99/00586
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.2
SEQ ID NO 24
LENGTH: 1422
TYPE: DNA
ORGANISM: homo sapiens
US-09-909-650B-24
Query Match 10.3%; Score 82.8; DB 3; Length 1422;
Best Local Similarity 97.7%; Pred. No. 4e-11;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GTACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTGCAATTC 685
DB 1283 GCACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTGCAATTC 1224
QY 686 ATTACTTCCTTGATAGATTTCTGT 711
DB 1223 ATTACTTCCTTGATAGATTTCTTT 1198
RESULT 2
US-09-130-616-178/c
Sequence 178, Application US/09130616C
Patent No. 6221850
GENERAL INFORMATION:
APPLICANT: McKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
FILE REFERENCE: ISPH-0318
CURRENT APPLICATION NUMBER: US/09/130,616C
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
EARLIER FILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 178
SEQ ID NO 178
LENGTH: 1505
TYPE: DNA
ORGANISM: Homo sapien
US-09-130-616-178

Query Match 10.3%; Score 82.8; DB 3; Length 1505;
Best Local Similarity 97.7%; Pred. No. 4.1e-11;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTGCAATTC 685
DB 1323 GCACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTGCAATTC 1264
QY 686 ATTACTTCCTTGATAGATTTCTGT 711
DB 1263 ATTACTTCCTTGATAGATTTCTTT 1238

RESULT 3

US-09-023-655-952/c
Sequence 952, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 952:
SEQUENCE CHARACTERISTICS:
LENGTH: 1505 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: G1463124
US-09-023-655-952
Query Match 10.3%; Score 82.8; DB 3; Length 1505;
Best Local Similarity 97.7%; Pred. No. 4.1e-11;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GTACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTGCAATTC 685
DB 1323 GCACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTGCAATTC 1264
QY 686 ATTACTTCCTTGATAGATTTCTGT 711

```

Db      1263 ATTACTTCTGTGATAGTTCCTT 1238

RESULT 4
US-09-165-522-1/c
; Sequence 1, Application US/09165522
; Patent No. 6943000
; GENERAL INFORMATION:
; APPLICANT: Davis, Roger J.
; Flavel, Richard A.
; Ratic, Pasko
; Whitmarsh, Alan
; Kuan, Chia-yi
; Yang, Di
;
; TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,522
; FILING DATE: 02-Oct-1998
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/060,995
; FILING DATE: 03-Oct-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 10363/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
;
; INFORMATION FOR SEQ ID NO: 1:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1505 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 68...1459
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-165-522-1

Query Match      10.3%; Score 82.8; DB 3; Length 1505;
Best Local Similarity 97.7%; Pred. No. 4,1e-11;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      626 GTACTGAAGGAGGAGGCTGTCCTTTTACTACACCATTTTAAAGTCTTTCTTCTGAATC 685
      |||
Db      1323 GCACCTGAAGGAGGAGGCTGTCCTTTTACTACACCATTTTAAAGTCTTTCTTGAATC 1264
      |||
QY      686 ATTACTTCTGTAGATAGTTCCTT 711
      |||
Db      1263 ATTACTTCTGTAGATAGTTCCTT 1238
      |||

RESULT 5
US-09-165-522-3/c
; Sequence 3, Application US/09165522
; Patent No. 6943000
; GENERAL INFORMATION:

```

```

1  APPLICANT: Davis, Roger J.
2  Playell, Richard A.
3  Rakic, Pasiko
4  Whitmarsh, Alan
5  Kuan, Chia-Yi
6  Yang, Di
7  TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
8  NUMBER OF SEQUENCES: 24
9  CORRESPONDENCE ADDRESS:
10 ADDRESS: Fish & Richardson P.C.
11 STREET: 225 Franklin Street
12 CITY: Boston
13 STATE: MA
14 COUNTRY: USA
15 ZIP: 02110-2804
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Diskette
18 COMPUTER: IBM Compatible
19 OPERATING SYSTEM: Windows 95
20 SOFTWARE: FastSeq for Windows Version 2.0b
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/09/165,522
23 FILING DATE: 02-Oct-1998
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: 60/060,995
26 FILING DATE: 03-Oct-1997
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Fasse, J. Peter
29 REGISTRATION NUMBER: 32,983
30 REFERENCE/DOCKET NUMBER: 10363/005001
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: 617/542-5070
33 TELEFAX: 617/542-8906
34 TELEX: 200154
35 INFORMATION FOR SEQ ID NO: 3:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 2367 base pairs
38 TYPE: nucleic acid
39 STRANDEDNESS: double
40 TOPOLOGY: linear
41 MOLECULE TYPE: DNA
42 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
43 US-09-165-522-3
44
45 Query Match 10.3%; Score 82.8; DB 3; Length 2367;
46 Best Local Similarity 97.7%; Pred. No. 4.6e-11;
47 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
48
49 QY 626 GTACCTGAAGAGAGAGCTGCTCTTTACTACACACATTTTACGCTTTCTTCGAAATTC 685
50 DB 1479 GCACCTGAAGAGAGAGCTGCTCTTTACTACACACATTTTACGCTTTCTTCGAAATTC 1420
51 QY 686 ATTACTCTCTGTAGATGATTCGT 711
52 DB 1419 ATTACTCTCTGTAGATGATTCGT 1394
53
54 RESULT 6
55 US-09-566-921-34/C
56 Sequence 34, Application US/09566921
57 Patent No. 6682888
58 GENERAL INFORMATION:
59 APPLICANT: Loring, Jeanne F.
60 APPLICANT: Tingley, Debora W.
61 APPLICANT: Edwards, Carla M.
62 TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
63 FILE REFERENCE: PA-0024 US
64 CURRENT APPLICATION NUMBER: US/09/566,921
65 CURRENT FILING DATE: 2000-05-05
66 NUMBER OF SEQ ID NOS: 138
67 SOFTWARE: PERL Program
68 SEQ ID NO 34
69 LENGTH: 2677

```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: incyle ID No. 6682888 413797.5
; NAME/KEY: unsure
; LOCATION: 2024
; OTHER INFORMATION: a, t, c, g, or other
US-09-566-921-34

Query Match
Best Local Similarity 97.7%; Pred. No. 4.8e-11;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAGAGAGAGGCTGTCTTACTACACCATTTTACTTCTTCTGCAATTC 685
DB 1795 GCACCTGAGAGAGAGGCTGTCTTACTACACCATTTTACTTCTTCTGCAATTC 1736

QY 686 ATTACTTCTTGTAGATAGTTCTGT 711
DB 1735 ATTACTTCTTGTAGATAGTTCTTT 1710

RESULT 7
US-09-909-650B-22/c
; Sequence 22, Application US/09909650B
; Patent No. 6649388
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Inc.
; APPLICANT: Fournier, Alain
; APPLICANT: Maury, Isabelle
; APPLICANT: Zhou-Liu, Qing
; APPLICANT: Desautels-Cremont, Francine
; TITLE OF INVENTION: Polypeptides Derived From JNK3
; FILE REFERENCE: ST99003-US-CNT-1
; CURRENT APPLICATION NUMBER: US/09/909,650B
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: PCT/FR00/00104
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/122,175
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: US 99/00586
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 22
; LENGTH: 1306
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-909-650B-22

Query Match
Best Local Similarity 10.1%; Score 80.4; DB 3; Length 1306;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAGAGAGAGGCTGTCTTACTACACCATTTTACTTCTTCTGCAATTCATTA 689
DB 1279 CTGAGAGAGAGGCTGTCTTACTACACCATTTTACTTCTTCTGCAATTCATTA 1220

QY 690 CTTCCTGTAGATAGTTCTGT 711
DB 1219 CTTCCTGTAGATAGTTCTTT 1198

RESULT 8
US-09-130-616-177/c
; Sequence 177, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Nero, Pam
```

```

; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; FILE REFERENCE: FOR THE MODULATION OF JNK PROTEINS
; FILE REFERENCE: ISPH-0318
; CURRENT APPLICATION NUMBER: US/09/130,616C
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 177
; LENGTH: 1773
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-130-616-177

Query Match
Best Local Similarity 10.1%; Score 80.4; DB 3; Length 1773;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAGAGAGAGGCTGTCTTACTACACCATTTTACTTCTTCTGCAATTCATTA 689
DB 1343 CTGAGAGAGAGGCTGTCTTACTACACCATTTTACTTCTTCTGCAATTCATTA 1284

QY 690 CTTCCTGTAGATAGTTCTGT 711
DB 1283 CTTCCTGTAGATAGTTCTTT 1262

RESULT 9
US-09-165-522-4/c
; Sequence 4, Application US/09165522
; Patent No. 6943000
; GENERAL INFORMATION:
; APPLICANT: Davis, Roger J.
; APPLICANT: Flavell, Richard A.
; APPLICANT: Rakic, Pasko
; APPLICANT: Whitmarsh, Alan
; APPLICANT: Kuan, Chia-Yi
; APPLICANT: Yang, Di
; TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,522
; FILING DATE: 02-Oct-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/060,995
; FILING DATE: 03-Oct-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 10363/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1773-base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
```

MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 92...1357
SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-09-165-522-4

Query Match 10.1%; Score 80.4; DB 3; Length 1773;
Best Local Similarity 98.8%; Pred. No. 1.7e-10;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTCTTTCTTCTGAAATTCATTA 689
DB 1343 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTCTTTCTTCTGAAATTCATTA 1284

QY 690 CTTCCTTTGATAGTAAGTTCTGT 711
DB 1283 CTTCCTTTGATAGTAAGTTCTTT 1262

RESULT 10
US-09-771-161A-87/c
Sequence 87, Application US/09771161A
Patent No. 6936450
GENERAL INFORMATION:
APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771.161A
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/774, 676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PatentIn version 3.0
SEQ ID NO 87
LENGTH: 2131
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: -
LOCATION: (1)..(2131)
OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'
US-09-771-161A-87

Query Match 10.1%; Score 80.4; DB 3; Length 2131;
Best Local Similarity 98.8%; Pred. No. 1.8e-10;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTCTTTCTTCTGAAATTCATTA 689
DB 1225 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTCTTTCTTCTGAAATTCATTA 1166

QY 690 CTTCCTTTGATAGTAAGTTCTGT 711
DB 1165 CTTCCTTTGATAGTAAGTTCTTT 1144

RESULT 11
US-09-130-616-174/c
Sequence 174, Application US/09130616C
Patent No. 6221850
GENERAL INFORMATION:
APPLICANT: McKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Mont, Brett
APPLICANT: Netro, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS

FILE REFERENCE: ISPH-0318
CURRENT APPLICATION NUMBER: US/09/130.616C
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
EARLIER FILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 178
SEQ ID NO 174
LENGTH: 2372
TYPE: DNA
ORGANISM: Homo sapiens
US-09-130-616-174

Query Match 10.1%; Score 80.4; DB 3; Length 2372;
Best Local Similarity 98.8%; Pred. No. 1.8e-10;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTCTTTCTTCTGAAATTCATTA 689
DB 1475 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTCTTTCTTCTGAAATTCATTA 1416

QY 690 CTTCCTTTGATAGTAAGTTCTGT 711
DB 1415 CTTCCTTTGATAGTAAGTTCTTT 1394

RESULT 12
US-09-016-434-1389/c
Sequence 1389, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1389:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9468150
US-09-016-434-1389

Query Match 10.1%; Score 80.4; DB 3; Length 2372;
Best Local Similarity 98.8%; Pred. No. 1.8e-10;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAGAGAGAGGCTGCTCTTTACTACACATTTTACTCTTCTCTGAAATTCATTA 689
DB 1475 CTGAGAGAGAGGCTGCTCTTTACTACACATTTTACTCTTCTCTGAAATTCATTA 1416

QY 690 CTTCCTGTAGATTAAGTTCTGT 711
DB 1415 CTTCCTGTAGATTAAGTTCTTT 1394

RESULT 13
US-09-165-522-6/c
Sequence 6, Application US/09165522
Patent No. 6943000
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
Flavell, Richard A.
Rakic, Paeko
Whitmarsh, Alan
Kuan, Chia-Yi
Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Faese, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-165-522-6

Query Match 10.1%; Score 80.4; DB 3; Length 2372;
Best Local Similarity 98.8%; Pred. No. 1.8e-10;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAGAGAGAGGCTGCTCTTTACTACACATTTTACTCTTCTCTGAAATTCATTA 689
DB 1475 CTGAGAGAGAGGCTGCTCTTTACTACACATTTTACTCTTCTCTGAAATTCATTA 1416

QY 690 CTTCCTGTAGATTAAGTTCTGT 711
DB 1415 CTTCCTGTAGATTAAGTTCTTT 1394

RESULT 14
US-09-165-522-7/c
Sequence 7, Application US/09165522
Patent No. 6943000
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
Flavell, Richard A.
Rakic, Paeko
Whitmarsh, Alan
Kuan, Chia-Yi
Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Faese, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 224...1489
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-165-522-7

Query Match 10.1%; Score 80.4; DB 3; Length 2372;
Best Local Similarity 98.8%; Pred. No. 1.8e-10;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAGAGAGAGGCTGCTCTTTACTACACATTTTACTCTTCTCTGAAATTCATTA 689
DB 1475 CTGAGAGAGAGGCTGCTCTTTACTACACATTTTACTCTTCTCTGAAATTCATTA 1416

QY 690 CTTCCTGTAGATTAAGTTCTGT 711
DB 1415 CTTCCTGTAGATTAAGTTCTTT 1394

RESULT 15
US-09-566-921-33/c
Sequence 33, Application US/09566921
Patent No. 6682888
GENERAL INFORMATION:
APPLICANT: Loring, Jeanne F.

	Query Match	8.3%;	Score 66.8;	DB 3.	Length 1975;
	Best Local Similarity	86.0%;	Pred. No. 4.4e-07;		
	Matches 74;	Conservative 0;	Mismatches 12;	Indels 0;	Gaps 0;
QY	626	GTACCTGAGGAGAAGCGCTGTCCTTTTACTACACCATTTTAGTCTTCTGAATC	685		
Dd	1505	GCACCTAAGGTAGGGGCTGGCCCTTTGACTACGCCGCTTCACTTGCTTCTGAGTTC	1446		
QY	686	ATTACTTCCTTGAGATAAGTTCTGT	711		
Dd	1445	ATTACTTCCTTGATGATGAGTTCTTT	1420		
RESULT 17					
US-09-165-522-9/c					
; Sequence 9, Application US/09165522					

```

RESULT 18
US-09-130-616-176/c
; Sequence 176, Application US/09130616C
; Patent No. 6221850
;
; GENERAL INFORMATION:
;
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monla, Brecht
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
;
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS

```

APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
FILE REFERENCE: ISPH-0318


```

; CURRENT APPLICATION NUMBER: US/09/130,616C
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 165
; LENGTH: 1408
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-130-616-165

Query Match
Best Local Similarity 74.4%; Score 50.8; DB 3; Length 1408;
Matches 64; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 626 GTACCTGAGAGAGAGGCTGTCTTTTACACACATTTTGTCTTTCTGAAATTC 685
DB 1317 GCACCTAAAGAGAGCGCTGCGCTTATGACGCCATTCTTAGTTCGCTCCCAATTC 1258
QY 686 ATTACTTCCTTTGATTAAGTTCTGT 711
DB 1257 ATGACCTCCTTGATATACAGTTCTTT 1232

RESULT 22
US-10-104-047-1930/C
; Sequence 1930, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1930
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1930

Query Match
Best Local Similarity 70.7%; Score 48.8; DB 3; Length 2372;
Matches 65; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 626 GTACCTGAGAGAGAGGCTGTCTTTTACACACATTTTGTCTTTCTGAAATTC 685
DB 1382 GCACCTAAAGAGAGGCGCTGCGCTTATGACGCCATTCTTAGTTCGCTCCCAATTC 1323
QY 686 ATTACTTCCTTTGATTAAGTTCTGTAAGAA 717
DB 1322 ATACTTCCTTATATATCATTCCTGTAAGAA 1291

RESULT 23
US-09-130-616-173/C
; Sequence 173, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monla, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
; FILE REFERENCE: ISPH-0318
; CURRENT APPLICATION NUMBER: US/09/130,616C
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
```

```

; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 173
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-130-616-173

Query Match
Best Local Similarity 74.4%; Score 48.4; DB 3; Length 1619;
Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGGCTGTCTTTTACACACATTTTGTCTTTCTGAAATTCATTA 689
DB 1172 CTGACCTGAGAGGCTATCTTTTACACACATTCCTTCTTCCCAATTCATGA 1113
QY 690 CTTCCTTTGATTAAGTTCTGT 711
DB 1112 CTTCCTTTGATTAAGTTCTTT 1091

RESULT 24
US-08-220-602B-17/C
; Sequence 17, Application US/08220602B
; Patent No. 6514745
; GENERAL INFORMATION:
; APPLICANT: KARIN, MICHAEL
; APPLICANT: DAVIS, ROGER
; APPLICANT: MASAHIKO, HIBI
; APPLICANT: ANNING, LIN
; APPLICANT: DERJARD, BENOIT
; TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/220,602B
; FILING DATE: 25-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.,
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07257/015001 (PD3205)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1780 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: JNK2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 59..1330
US-08-220-602B-17

Query Match
Best Local Similarity 74.4%; Score 48.4; DB 3; Length 1780;
Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
```


SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-861-097-17

Query Match 6.0%; Score 48.4; DB 3; Length 1780;
Best Local Similarity 74.4%; Pred. No. 0.017;

Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTCTACTACACCATTTTGTCTTCTTCTGATTCATTA 689
DB 1196 CTGCATCTGAAGGCTGATCTTTTACACACCATTTCTTCTTCCATTCATGA 1137

OY 690 CTTCCTGTAGATTAAGTCTGT 711
DB 1136 CTTCCTGTAAATTAAGCTCTTT 1115

RESULT 28

PCT-US94-12913A-17/c

Sequence 17, Application PC/RUS9412913A

GENERAL INFORMATION:

APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

APPLICANT: KARIN, MICHAEL

APPLICANT: DAVIS, ROGER

APPLICANT: HIBI, MASAHIKO

APPLICANT: LIN, ANNING

TITLE OF INVENTION: ONCOROTHEIN PROTEIN KINASE

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ

STREET: 1880 CENTURY PARK EAST, SUITE 500

CITY: LOS ANGELES

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 90067

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/12913A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/08119

FILING DATE: 18-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: LISA A. HAILE, PH.D.

REGISTRATION NUMBER: P-38,347

REFERENCE/DOCKET NUMBER: FD-1205

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 455-5100

TELEFAX: (619) 455-5110

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 1780 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

IMMEDIATE SOURCE:

CLONE: JNK2

FEATURE:

NAME/KEY: CDS

LOCATION: 59..1330

PCT-US94-12913A-17

OY 630 CTGAAGAGAGAGGCTGCTCTTCTACTACACCATTTTGTCTTCTTCTGATTCATTA 689
DB 1196 CTGCATCTGAAGGCTGATCTTTTACACACCATTTCTTCTTCCATTCATGA 1137

OY 690 CTTCCTGTAGATTAAGTCTGT 711
DB 1136 CTTCCTGTAAATTAAGCTCTTT 1115

RESULT 29

US-09-209-668-16/c

Sequence 16, Application US/09209668A

Patent No. 6114517

GENERAL INFORMATION:

APPLICANT: MONIA, BRETT P.

APPLICANT: XU, XIAOXING S.

TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR

FILE REFERENCE: ISPH-0316

CURRENT APPLICATION NUMBER: US/09/209,668A

CURRENT FILING DATE: 1998-12-10

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 16

LENGTH: 1782

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (59)..(1333)

PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: U13951/Genbank

DATABASE ENTRY DATE: 1994-12-06

US-09-209-668-16

Query Match 6.0%; Score 48.4; DB 3; Length 1782;
Best Local Similarity 74.4%; Pred. No. 0.017;

Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

OY 630 CTGAAGAGAGAGGCTGCTCTTCTACTACACCATTTTGTCTTCTTCTGATTCATTA 689
DB 1196 CTGCATCTGAAGGCTGATCTTTTACACACCATTTCTTCTTCCATTCATGA 1137

OY 690 CTTCCTGTAGATTAAGTCTGT 711
DB 1136 CTTCCTGTAAATTAAGCTCTTT 1115

RESULT 30

US-09-130-616-169/c

Sequence 169, Application US/09130616C

Patent No. 6221850

GENERAL INFORMATION:

APPLICANT: MCKAY, ROBERT A.

APPLICANT: DEAN, NICHOLAS M.

APPLICANT: MONIA, BRETT

APPLICANT: NERO, PAM

TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS

FILE REFERENCE: ISPH-0318

CURRENT APPLICATION NUMBER: US/09/130,616C

CURRENT FILING DATE: 1998-08-07

EARLIER APPLICATION NUMBER: 08/910,629

NUMBER OF SEQ ID NOS: 178

SEQ ID NO 169

LENGTH: 1782

TYPE: DNA

ORGANISM: Homo sapiens

US-09-130-616-169

Query Match 6.0%; Score 48.4; DB 3; Length 1782;

Best Local Similarity 74.4%; Pred. No. 0.017;
Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 630 CTGAGAGAGAGAGGCTGCTCTTTACTACACCATTTTACTTTCTTCTTGAATTCATTA 689
1196 CTGACATCTGAAGGCTGATCTTTTACACACATCTTGCTCTTCTTCCCAATCCATGA 1137
QY 690 CTTCCTGTAGTAACTTCTGT 711
1136 CTTCCTGTAAATTAAGCTCTT 1115
Db 1136 CTTCCTGTAAATTAAGCTCTT 1115
RESULT 31
US-09-949-016-13750/C
Sequence 13750, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13750
LENGTH: 132456
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(132456)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13750
Query Match
Best Local Similarity 71.1%; Pred. No. 0.055;
Matches 64; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 628 ACCTGAGAGAGAGGCTGCTCTTTACTACACCATTTTACTTTCTTCTTGAATTCAT 687
126588 ACCTAAGAGAGAGGCTGCCCCCGTATTAATCTCATCTTGCTCTCCCAAGTCAT 126529
Db 126588 ACCTAAGAGAGGCTGCCCCCGTATTAATCTCATCTTGCTCTCCCAAGTCAT 126529
QY 688 TACTTCTGTAGTAACTTCTGTAGAAA 717
126528 AACTTCTGTATATATCAATTTCTTAAAGA 126499
Db 126528 AACTTCTGTATATATCAATTTCTTAAAGA 126499
RESULT 32
US-09-130-616-171/C
Sequence 171, Application US/09130616C
Patent No. 6221850
GENERAL INFORMATION:
APPLICANT: McKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
FOR THE MODULATION OF JNK PROTEINS
FILE REFERENCE: ISPH-0318
CURRENT APPLICATION NUMBER: US/09/130,616C
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 08/910,629
PRIOR FILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 178
SEQ ID NO 171

LENGTH: 1392
TYPE: DNA
ORGANISM: Homo sapiens
US-09-130-616-171
Query Match
Best Local Similarity 5.8%; Score 46.8; DB 3; Length 1392;
Matches 57; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 638 GAAGGCTGCTCTTTACTACACCATTTTACTTTCTTCTTGAATTCATTTCTCTTG 697
1174 GAAGGCTGATCTTTTACACACATCTTGCTCTTCTTCCCAATCCATGACTTCTTG 1115
Db 1174 GAAGGCTGATCTTTTACACACATCTTGCTCTTCTTCCCAATCCATGACTTCTTG 1115
QY 698 TAGATAGTCTGT 711
1114 TAAATTAAGCTCTT 1101
Db 1114 TAAATTAAGCTCTT 1101
RESULT 33
US-09-023-655-953/C
Sequence 953, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 953:
SEQUENCE CHARACTERISTICS:
LENGTH: 1392 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 91463128
US-09-023-655-953
Query Match
Best Local Similarity 5.8%; Score 46.8; DB 3; Length 1392;
Matches 57; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 638 GAAGGCTGCTCTTTACTACACCATTTTACTTTCTTCTTGAATTCATTTCTCTTG 697
1174 GAAGGCTGATCTTTTACACACATCTTGCTCTTCTTCCCAATCCATGACTTCTTG 1115
Db 1174 GAAGGCTGATCTTTTACACACATCTTGCTCTTCTTCCCAATCCATGACTTCTTG 1115

Db 1174 GAAGGCTGCTTTTACACACCATCTGCTCTTCTTCCCAATCAGTACTTCTTG 1115
| | | | |
Qy 698 TAGATAGTCTGT 711
| | | | |
Db 1114 TAAATTAGCTCTT 1101

RESULT 34
US-09-949-016-5346/c
; Sequence 5346, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5346
; LENGTH: 1392
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5346

Query Match 5.8%; Score 46.8; DB 3; Length 1392;
Best Local Similarity 77.0%; Pred. No. 0.041; Indels 0; Gaps 0;
Matches 57; Conservative 0; Mismatches 17;
Qy 638 GAAGGCTGCTTTTACTACACCATTTTACTGCTCTTCTTCTGATTCATTACTCTTG 697
| | | | |
Db 1174 GAAGGCTGATCTTTTACAACACCATCTTCTTCTTCCCAATCAGTACTTCTTG 1115
| | | | |
Qy 698 TAGATAGTCTGT 711
| | | | |
Db 1114 TAAATTAGCTCTT 1101

RESULT 35
US-09-130-616-172/c
; Sequence 172, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monla, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
; FILE REFERENCE: ISPR-0318
; CURRENT APPLICATION NUMBER: US/09/130,616C
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 172
; LENGTH: 1523
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-130-616-172

Query Match 5.8%; Score 46.8; DB 3; Length 1523;
Best Local Similarity 77.0%; Pred. No. 0.042; Indels 0; Gaps 0;
Matches 57; Conservative 0; Mismatches 17;

Qy 638 GAAGGCTGCTTTTACTACACCATTTTACTGCTCTTCTTCTGATTCATTACTCTTG 697
| | | | |
Db 1152 GAAGGCTGATCTTTTACAACACCATCTTCTTCTTCCCAATCAGTACTTCTTG 1093
| | | | |
Qy 698 TAGATAGTCTGT 711
| | | | |
Db 1092 TAAATTAGCTCTT 1079

RESULT 36
US-08-253-155A-19/c
; Sequence 19, Application US/08253155A
; Patent No. 5691147
; GENERAL INFORMATION:
; APPLICANT: Gyuris, Jeno
; APPLICANT: Diaretta, Giulio
; TITLE OF INVENTION: CDK4 Binding Proteins
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,155A
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MII-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1769 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-253-155A-19

Query Match 5.8%; Score 46.8; DB 2; Length 1769;
Best Local Similarity 77.0%; Pred. No. 0.043; Indels 0; Gaps 0;
Matches 57; Conservative 0; Mismatches 17;
Qy 638 GAAGGCTGCTTTTACTACACCATTTTACTGCTCTTCTTCTGATTCATTACTCTTG 697
| | | | |
Db 1012 GAAGGCTGATCTTTTACAACACCATCTTCTTCTTCCCAATCAGTACTTCTTG 953
| | | | |
Qy 698 TAGATAGTCTGT 711
| | | | |
Db 952 TAAATTAGCTCTT 939

RESULT 37
US-09-016-434-1437/c
; Sequence 1437, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1437:
SEQUENCE CHARACTERISTICS:
LENGTH: 1873 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 5607785
US-09-016-434-1437

Query Match 5.8%; Score 46.8; DB 3; Length 1873;
Best Local Similarity 73.2%; Pred. No. 0.044;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 630 CTGAGAGAGAGGCTGCTTCTTACTACACCATTTTCTTCTTCTGCAATTATTA 689
DB 1289 CTGCATCTGAGAGCTGATCTTTTACACACCATTTCTTCTTCTCCATCATGA 1230
QY 690 CTTCCCTGTAGATAGTCTGT 711
DB 1229 CTTCTTTGTAAATTAAGTCTTTT 1208

RESULT 38
US-09-949-016-53117/c
Sequence 53117, Application US/09949016
Patent No. 6812338
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIORITY FILING DATE: 2000-04-14
PRIORITY APPLICATION NUMBER: 60/241,755
PRIORITY FILING DATE: 2000-10-20
PRIORITY APPLICATION NUMBER: 60/237,768
PRIORITY FILING DATE: 2000-10-03
PRIORITY APPLICATION NUMBER: 60/231,498
PRIORITY FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 53117
LENGTH: 601
TYPE: DNA

ORGANISM: Human
US-09-949-016-53117

Query Match 5.8%; Score 46; DB 3; Length 601;
Best Local Similarity 54.0%; Pred. No. 0.051;
Matches 94; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 389 ATTACTATTAAATTTATTTATGAAAAAGTTTGTCTGGATCATTTACATGAAATAT 448
DB 519 AATACTTTTAAATTTGTTTTTTTAAACATTTTACACATGAAAAATATCTTTTCTACAT 460
QY 449 CAGATGATGCCACACGACGAAATATCAAGAAATTAATCATTTATAGACACAA 508
DB 459 TTAACAGATGTGACTTAAACATTTGACATATACACATATGCAATTAATAGCAATA 400
QY 509 ACCATGTGATATTTGTCATCTGCTTTTAAAGCAATGTATTTCTTCA 562
DB 399 ABAATGACTTATTTCTTCATCTGGCTTAATCTTAAGTCAATATCTTGA 346

RESULT 39
US-09-806-708B-22
Sequence 22, Application US/09806708B
Patent No. 6784342
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
PRIORITY FILING DATE: 2001-04-03
PRIORITY APPLICATION NUMBER: US 60/147,133
PRIORITY FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patent in version 3.0
SEQ ID NO 22
LENGTH: 1141
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(1141)
OTHER INFORMATION: consensus sequence of A.T., L.a., and B.n. FAEI promoters
US-09-806-708B-22

Query Match 5.8%; Score 46; DB 3; Length 1141;
Best Local Similarity 11.0%; Pred. No. 0.061;
Matches 85; Conservative 284; Mismatches 400; Indels 2; Gaps 2;

QY 18 TTATAGTAGAGCATAGCTCTTAGAAAAAATATATAGCATTAATAGTAATGTCTC 77
DB 115 TTKMGKTGMRHRWYWRAMBTDVHHVYTAANNATTCMDKDKRTTMMKKNNATG 174
QY 78 AAGTACTATAAGACATTAAGATGATGATTAATAATATATATGAC -AATGTGTAT 136
DB 175 WDDTKYHMMNNNGBYTWTWVRYKTDMSBKRNNGMBWKKMSYDVTYWWWDDMC 234
QY 137 TAGATCTGTGCTGACGACAAAGAAAATTTTCAAGCTGACCTTAAACGAGCCATCTT 196
DB 235 KKKYRWRTGTRMRNYYVAMBTAHRRYNNGWTBAMVRYRTWNNNNNNNAAAMCRARY 294
QY 197 GGTATGTTTCAATATATTTGCACATCAACCTTGAAGAGTCAACACTAAGATGAA 256
DB 295 WGMNBAVNSTCTTWKSKTKTKVRSWMNCRAGDANKDKMKMSAAGVYWNNNNNN 354
QY 257 TGAGGAGAGGTAGCGGCTGAAGAGATTAGTCACTGACATTAAGTGTGATGTCATAA 316
DB 355 WYKKAABHABDWVWHSAMKMHANAHSKKTBYKRTKTVNNNNNGTTWKKMWAWY 414
QY 317 GGGCATTTATGGCTGGAATTTTGAAGAGCATTTACCTTTAGCCCATGTTAACATT 376
DB 415 WMDMDWEGTYNNNNNGRTYTGWTNKKMTYTKNNCCNRAMDKTKTHNNNTWKK 474
QY 377 TCTCAGATTCATTACTATTAAATTTATTATGAAAAAGTTTGTCTGGATCATTTAC 436

```

Db      475 MKTYMNNCYKSMWNGKSHREAAVVTWYMWMMRRYAHANNNNNDYWMKQCTWYKYVCS 534
      437 CATGAGAATAATCGAATGAATGCCACGTAATATCAAAAGAAATTAATAATCAT 496
      535 KMMNNYAAWYTKSSWNTSRYYRWKTNWSWERSDTSMGANNYAABHGYKMTNRMW 594
      497 TATAAGACACAACCATGTGATATTTGTCATCGCTGCTTAAAGCAATGTATGTATTT 556
      595 BMSHTHEBERAGAAHYMBMBYBAKCMKAMWYAKKYAGAGSGSNNNNNNNNNNNNNN 654
      557 CTTCGACCCCTACACAAAGGCCAAGAAATTAACAAGTACTAGTTATTTGTTATTCAC 616
      655 ATCABDDYAAASRYAAANAKWYKYBAANNAAYTHANNWGCNNATDTRRTWKNNNN 714
      617 GGAGAGTACTGTA-AGAGAAAGCTGCTCTTTACTACACCAATTTTACTGCTTTC 675
      715 NNAGTWNNNNNNAKNASAKNYAAAAYKAAKHMWRANKMAGMHADAABTTDKRN 774
      676 TTCTGAATTCATTACTCTTGTAGTAAGTCTGTAGAAACAGCTGTGTTATATAGA 735
      775 GAYTKTTTNNNNYRGVNTNTAARDGMANNNNNNNNNNNNNGMSDMWVTWYAYVGT 834
      736 AAACAATTATCTCTTCATCCACAGGAAATTCATTAATCCCAATA 786
      835 NNNNNNNNNYAMWTKWYTTDDRRWRBAVYTNNNNNNNRMAYYGAYADYA 885

```

```

RESULT 40
US-09-806-708B-22/c
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.T., L.A., and B.N. FAE1 promoters
US-09-806-708B-22

```

```

Query Match      5.8%; Score 46; DB 3; Length 1141;
Best Local Similarity 11.9%; Pred. No. 0.061;
Matches 86; Conservative 241; Mismatches 393; Indels 5; Gaps 1;

QY      71 TTGTCCAGTCTACTAAGACATTAAGTACAGTAAATAATATATATGACAAATT 130
      1128 TTKTKYKAKNNNNNNNNNGKMDNNRMDATKYSATGTAWMTNNAKRAATKCMYWTGTR 1069
      131 GTGTATTAGATCTGTGGCTAGCAAGAAATTTTCCAGCTGACCTTAACCGAGCC 190
      1068 RMCMTYYAARTWTRBSNANMSCATKEMWTKMYATKRYRAWYAMMCAMNNNNMCATNG 1009
      191 CATCTTGGTATGTTTCAACTATTTGTACATCAACCTTGAGAAAGTTCAAACTAAG 250
      1008 YAKSCATNNAMWATTRMAAAYAAAKARAVAGNNMRMYGAAGNKMGCMAMATMGBMWAD 949
      251 AATGATGAGGGAAGGTAGCGCTGAAGAATTAAGTACGCTCCACATGATGATGAG 310
      948 TKGKMCNNNNNNNTTDDRRAAMAKNNNNNNNAAYTACVYNPAATNNKATHTMKWTHGAHS 889
      311 TCAAAAGGCAATTAGGCTCTGAATTTTGATGAGGACATTTACCTTTAGCCCATGTTA 370

```

```

Db      888 KRTREHTRCRRTKXNNNNNNNAATYVYWHABRBMAMWTRTNNNNNNNNNNACSNTR 829
      371 ACATTTTCTTCAGAGTTCATTAATTAATTAATTAAGAAAAGTTTTCCTGGAT 430
      828 TWAABWBSGKNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 769
      431 CATTAACATCAGATATATAGCAATGCAATGCAACAGTAATGCAAAAGAAATAAATA 490
      768 AVTTHTDWCYKTWNTTWMDMTWBTBTTTTRNNNTSTNNNTNNNNNNNNNNNNNNNN 709
      491 AATCATTAATAGACACAACATGATATTTGTCATCGCTCTTAAAGCAATGTTATG 550
      708 KAYYAAATNNWG-----CMNNNTDARTNNNTTYMRBRMMNTNTTRYSTRRHHYGTATN 654
      551 TTAATTTCTGCAACCCCTACACAAAGGCCAAGAAATTAACAAGTACTAGTTATG 610
      653 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 594
      611 ATTCAGGAGAGTACTCTGAGAGAAAGCTGCTTTTACTACACCATTTTATAGTC 670
      593 WYANMRCSDVYTRNNNTCKSYAHSYWYNNAMWYRBYSAARNWSMARWTRNNNNWS 534
      671 TTTCTTCTGAATTCATTACTCTCTGTAGTATGTTGTAAGAAACAGCTGTATAT 730
      533 GBVBRMAGTMMWRHNNNNNTDTRYYWYKWARBTYYVDSGNKAKSMRGNMRAMKM 474
      731 ATGAAAACAAATTTATCTTCATCCACAGGAAATTCATTAATGCAAAATTA 790
      473 WMAANNDAAGMDHWTWMMGNNTWMMRBAKMMMAACBRAYCCNNNNNNBACVHKKMMR 414
      791 CGTT 795
      413 WTKY 409

```

```

RESULT 41
US-09-949-016-13276
; Sequence 13276, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13276
; LENGTH: 100877
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: (1)..(100877)
; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-13276

```

```

Query Match      5.8%; Score 46; DB 3; Length 100877;
Best Local Similarity 54.0%; Pred. No. 0.2;
Matches 94; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY      389 ATTACTATTAAATATTATTAAGAAAGTTTGTGCTCGATCATTAAGATTAAT 448
      14071 AATACTTTTAAATGTTTATTTTAAACAATTTTACATGAAAAAATATCTTTCTACAT 14130

```

QY	Db	QY	Db
449	CAGATAAATGCCACATGAAATACAAAGAAATAAAACCTTTAAGACAC	509	ACCATGTATTTGTGCATCTGCTTTTAAGCAATATATTTATCTTGA
14131	TAAACAGATGTGCTAAAAACATGACATATACAAATATGCTCAAAATTAAGCAATA	14191	AAATATGACTTATTTCTCATCTGTGGCTATATACCTAACTAAGTGAATACCTGAA

RESULT 42
 US-09-949-016-53116/c
 : Sequence 53116 Application US/09949016
 : Patent No. 6812339
 : GENERAL INFORMATION:
 : APPLICANT: VENTER, J. Craig et al.
 : TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 : TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 : FILE REFERENCE: CL001307
 : CURRENT APPLICATION NUMBER: US/09/949,016
 : CURRENT FILING DATE: 2000-04-14
 : PRIOR APPLICATION NUMBER: 60/241,755
 : PRIOR FILING DATE: 2000-10-20
 : PRIOR APPLICATION NUMBER: 60/237,768
 : PRIOR FILING DATE: 2000-10-03
 : PRIOR APPLICATION NUMBER: 60/231,498
 : PRIOR FILING DATE: 2000-09-08
 : NUMBER OF SEQ ID NOS: 207012
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 53116
 : LENGTH: 601
 : TYPE: DNA
 : ORGANISM: Human
 : US-09-949-016-53116

	Query Match	5.7%	Score 45.6	DB 3	Length 601
	Best Local Similarity	53.4%	Pred. No. 0.065	Mismatches 80	Indels 0
	Matches 93	Conservative 1		Gaps 0	
QY	389 ATTACTATTAATAATTATTTATGAAAAAGTTTTGTCCTGATCATTCACATCAGAAATAT				448
Db	470 AATCTTTTAAATTTGTTTTTTTAAACATTTTTACACATGAAAAATATCTTTTTCACAT				411
QY	449 CAGAAATGATCCACACTGTAATATCAAAAGAAATATAAACTAAATTCATTATAGACACA				508
Db	410 TAAACAGATGTGACTAAAAACATGACATATACCAACATATGACATCAAAAATATAGCAAAATA				351
QY	509 ACCATGTGATATTTGTCCATCGCTCTTTAAGCAATGTTATTTATCTTGCA				562
Db	350 AAAATGACTTATTTCTTCATCTGGGCTAATACCTACATGTCGAATATCTGAA				297

```

RESULT 43
US-09-621-976-2813/c
: Sequence 2813, Application US/09621976
: Patent No. 6639063
: GENERAL INFORMATION:
: APPLICANT: Dumas Milne Edwards, J.B.
: APPLICANT: Jobert, S.
: APPLICANT: Giordano, J.Y.
: TITLE OF INVENTION: ESTs and Encoded Human Proteins
: FILE REFERENCE: GENSET.054PR2
: CURRENT APPLICATION NUMBER: US/09/621,976
: CURRENT FILING DATE: 2000-07-21
: NUMBER OF SEQ. ID NOS: 19335
: SOFTWARE: Patent.pm
: SEQ. ID NO.2813
: LENGTH: 832
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 235..399
: US-09-621-976-2813

```

Query Match	5.6%	Score 44.6	DB 3	length 832
Best Local Similarity	17.7%	Pred. No. 0.13		
Matches	59	Conservative 125	Mismatches 149	Indels 0
			Gaps	0
Qy	462	ACACTGATATACAAAGATAAACTAAATCATTTATAGACACAACCGTGTGATTT	521	
Db	431	ACTTTGACTATGAACTAACTCCAGATTGCTAAAGTACAAAGAAATTGTACATAATATT	372	
Qy	522	TGTCATCTGCTCTTTAAGCAATGTATGTTATTTCTTGCAACCCCTACACAAAGCCA	581	
Db	371	ATATTGTTGYTMMWKKMMWYTTJTWIRMMMKKKARMMYMMKSTACASRYKRYTGW	312	
Qy	582	GAATTCACACAGACTAGTTATTGGTTATTCACGAGATGCTACCTGAAGAGAAAG	641	
Db	311	WYWMKKMMSTIRWYCYWCKKCCMYRGRCAWYIMARBRMMSYAMGRKKSMSMSMCTRM	252	
Qy	642	GCTGTCCTTTACTACACAACTTTTACTCTTTCTTCGTAATTCATTACTCTCTTGAGA	701	
Db	251	YKKGSYYTMWTKCTCATWICYWYMKYMRMMSKITCWSGSGYMTSYSTRSYSMYASMM	192	
Qy	702	TAACTTCTGAAGAAACAGCTGTGTTTATATAGAAAACAAATTTATCTTCCTCATCCACAG	761	
Db	191	YTMCMWMMGRMWSYTWYAMGKKWRYATTIRRRAMMMWMAAMTMMYMMWMMWMSRGLAM	132	
Qy	762	GAATTCATTACTTAATGCAAAATTAATTAAGTT	794	
Db	131	YRRTMMMGYRYYMRKKSYYRTRCAMAAYAKTK	99	

```

RESULT 44
US-09-130-616-168/c
: Sequence 168, Application US/09130616C
: Patent No. 6221850
: GENERAL INFORMATION:
: APPLICANT: McKay, Robert A.
: APPLICANT: Dean, Nicholas M.
: APPLICANT: Monia, Brett
: APPLICANT: Nero, Pam
: APPLICANT: Gaarde, William A.
: TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
: TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
: FILE REFERENCE: ISPH-0318
: CURRENT APPLICATION NUMBER: US/09/130.616C
: CURRENT FILING DATE: 1998-08-07
: EARLIER APPLICATION NUMBER: 08/910.629
: EARLIER FILING DATE: 1997-08-03
: NUMBER OF SEQ ID NOS: 178
: SEQ ID NO. 168
: LENGTH: 1349
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-130-616-168

```

	Query Match	Best Local Similarity	5.5%;	Score 44.4;	DB 3;	Length 1349;
	Matches	66;	Conservative	0;	Mismatches	26;
					Indels	0;
					Gaps	0;
QY	626	GTACACGAGAGAGAGGCTCTCTTTACACACACATTTTAACTCTTCTTCGAAATC				685
Db	1155	GCACTTAAGAGAGAGGAGCTGCCCCGATATTCATCTTGTGTTCTCTCCAAAGTC				1096
QY	686	ATTACTTCTCTTAGATTAAGTTCTGT				711
Db	1095	ATAACTTCCTATATATCAATTCCTTT				1070

RESULT 45
US-09-130-616-166/C
Sequence 166, Application US/09130616C
Patent No. 6221850
GENERAL INFORMATION:
APPLICANT: McKAY, Robert A.

APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
FILE REFERENCE: ISPH-0318
CURRENT APPLICATION NUMBER: US/09/130.616C
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910.629
EARLIER FILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 178
SEQ ID NO 166
LENGTH: 1365
TYPE: DNA
ORGANISM: Homo sapiens
US-09-130-616-166

Query Match 5.5%; Score 44.4; DB 3; Length 1365;
Best Local Similarity 69.8%; Pred. No. 0.16; Mismatches 26; Indels 0; Gaps 0;
Matches 60; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTTTCTTCTGAATTC 685
DB 1154 GCACCTAAGAGAGAGGCTGCCCCGTATACATCATTCTGTTCTCTCTCCAACTCC 1095

QY 686 ATTACTCTCTTGATGATTAAGTTCTGT 711
DB 1094 ATACTCTCTTATATATCAATCTTT 1069

RESULT 46
US-09-016-434-1139/C
Sequence 1139, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016.434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1139:
SEQUENCE CHARACTERISTICS:
LENGTH: 1365 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: G1463130
US-09-016-434-1139

Query Match 5.5%; Score 44.4; DB 3; Length 1365;
Best Local Similarity 69.8%; Pred. No. 0.16; Mismatches 26; Indels 0; Gaps 0;
Matches 60; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGCTCTTTACTACACCATTTTACTTTCTTCTGAATTC 685
DB 1154 GCACCTAAGAGAGAGGCTGCCCCGTATACATCATTCTGTTCTCTCTCCAACTCC 1095

QY 686 ATTACTCTCTTGATGATTAAGTTCTGT 711
DB 1094 ATACTCTCTTATATATCAATCTTT 1069

RESULT 47
US-09-621-976-2813
Sequence 2813, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621.976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 235..399
US-09-621-976-2813

Query Match 5.3%; Score 42.4; DB 3; Length 832;
Best Local Similarity 16.6%; Pred. No. 0.45; Mismatches 154; Indels 10; Gaps 1;
Matches 63; Conservative 153; Mismatches 154; Indels 10; Gaps 1;

QY 63 TAAGTAAATTGTCAGATCATCTAAGACATTAAGATGATCAAGTAAATATATAT 122
DB 25 YMMWMMKMYMKTYMWRBRKKKAMWKMTWTWYWRVYMWGTYKKKAKRTKKKKK 84

QY 123 GCACATTTGTGATTAAGATTCTGTGGCTAGCAAGAAATTTTCCAAGCTGACCTTAA 182
DB 85 GYMMWMMWMMRSYAMMTWTGTGAYYRSMYMMWRMRKKAAYRKTTCYSSKGMTW 144

QY 183 CCGAGGCCATCTTGATGATTTCA-----ACTATGTCATCAACCTTGAG 232
DB 145 KKKKAAWTTMMKTYMATAATRYMMWMCYTKRMRASWYCMWGGKRRKSTRKSSYS 204

QY 233 AAGAGTTCAACCTAAGATGAATGAGGAGAGGATAGCGCTGAAGAGATTACTGAGC 292
DB 205 AASARCCVCSGWSGMSMKYMMWRMRGMAATGAGKAMRBASCMWRKRYAGSKTSYGS 264

QY 293 TCACATTTGATGATGTCGATGATGTCGATGATGTCGATGATGTCGATGATGATG 352
DB 265 WMCWTRSMKYCYTKAWTGYCYRKGWGGKRWYASRKYMKWMMWMAWRYSTGT 324

QY 353 ACCCTTGAGCATGTTAAGATTTCTCAGGATTCATTAATTAATTAATTAATTAAT 412
DB 325 RASMMWRMYTMMKMKYAWARAAMWMAWMAWRAACAAATATATATTTATGTGT 384

QY 413 AAGTTTGTCTCTGATCA 432
DB 385 ACAATCTTGATCTTAGCA 404

```
RESULT 48
US-09-130-616-167/C
; Sequence 167, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; FILE REFERENCE: ISPH-0318
; CURRENT APPLICATION NUMBER: US/09/130,616C
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 167
; LENGTH: 1311
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-130-616-167

Query Match
Best Local Similarity 5.2%; Score 42; DB 3; Length 1311;
Best Local Similarity 69.5%; Pred. No. 0.63;
Matches 57; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTGCTTTCTTCTGAATTCATTA 689
DB 1156 CTAAAGAGAGGGCTGCCCCCGTATACATCTTGTTCTCTCCCAAGTCATTA 1097
QY 690 CTTCCTTGAGTAACTTCTGT 711
DB 1096 CTTCCTTATATATCAATTCCTT 1075

RESULT 49
US-09-209-668-14/C
; Sequence 14, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
; FILE REFERENCE: ISPH-0316
; CURRENT APPLICATION NUMBER: US/09/209,668A
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 1418
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (19)..(1173)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: L26318/Genbank
; DATABASE ENTRY DATE: 1994-04-25
US-09-209-668-14

Query Match
Best Local Similarity 5.2%; Score 42; DB 3; Length 1418;
Best Local Similarity 69.5%; Pred. No. 0.65;
Matches 57; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTGCTTTCTTCTGAATTCATTA 689
DB 1156 CTAAAGAGAGGGCTGCCCCCGTATACATCTTGTTCTCTCCCAAGTCATTA 1097
```

```
QY 690 CTTCCTTGAGTAACTTCTGT 711
DB 1096 CTTCCTTATATATCAATTCCTT 1075

RESULT 50
US-09-130-616-164/C
; Sequence 164, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; FILE REFERENCE: ISPH-0318
; CURRENT APPLICATION NUMBER: US/09/130,616C
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 164
; LENGTH: 1418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-130-616-164

Query Match
Best Local Similarity 5.2%; Score 42; DB 3; Length 1418;
Best Local Similarity 69.5%; Pred. No. 0.65;
Matches 57; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTGCTTTCTTCTGAATTCATTA 689
DB 1156 CTAAAGAGAGGGCTGCCCCCGTATACATCTTGTTCTCTCCCAAGTCATTA 1097
QY 690 CTTCCTTGAGTAACTTCTGT 711
DB 1096 CTTCCTTATATATCAATTCCTT 1075
```

Search completed: July 19, 2006, 20:14:12
Job time : 207 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2006, 19:12:50 ; Search time 1474 Seconds
(without alignments)
6669.002 Million cell updates/sec

Title: US10723681MOD.SEQ

Perfect score: 800
Sequence: 1 aacatttcacaaactctta.....caataatcagcttgatcg 800

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications NA Main:

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	798.4	99.8	76500	10 US-10-723-681-2	Sequence 2, Appli
2	798.4	99.8	110950	10 US-10-857-780-2	Sequence 2, Appli
3	796.8	99.6	2669	4 US-09-925-065A-683710	Sequence 683710,
4	796.8	99.6	2669	4 US-09-925-065A-683711	Sequence 683711,
5	796.8	99.6	2669	4 US-09-925-065A-683712	Sequence 683712,
6	796.8	99.6	2669	5 US-09-925-065A-683710	Sequence 683710,
7	796.8	99.6	2669	5 US-09-925-065A-683711	Sequence 683711,
8	796.8	99.6	2669	5 US-09-925-065A-683712	Sequence 683712,
9	463.4	57.9	823	10 US-10-857-780-4942	Sequence 4942, Ap
10	463.4	57.9	823	10 US-10-857-780-4943	Sequence 4943, Ap
11	456.4	57.0	572	4 US-09-925-065A-44644	Sequence 44644, A
12	456.4	57.0	572	4 US-09-925-065A-44644	Sequence 44644, A
13	456.4	57.0	572	12 US-10-301-480-145882	Sequence 145882,
14	456.4	57.0	572	12 US-10-301-480-145882	Sequence 145882,
15	82.8	10.3	1422	3 US-09-909-650A-23	Sequence 23, Appli
16	82.8	10.3	1505	3 US-09-165-522-1	Sequence 1, Appli
17	82.8	10.3	1505	8 US-10-641-643-952	Sequence 952, App

18	82.8	10.3	1505	8 US-10-343-710-56	Sequence 56, Appli
19	82.8	10.3	1505	16 US-11-180-044-1	Sequence 1, Appli
20	82.8	10.3	2211	15 US-11-180-817-10	Sequence 10, Appli
21	82.8	10.3	2367	3 US-09-165-522-3	Sequence 3, Appli
22	82.8	10.3	2367	16 US-11-180-044-3	Sequence 3, Appli
23	82.8	10.3	2677	10 US-10-765-700-34	Sequence 34, Appli
24	82.8	10.3	2698	15 US-11-127-817-11	Sequence 11, Appli
25	80.4	10.1	922	10 US-10-450-763-29386	Sequence 29386, A
26	80.4	10.1	999	10 US-10-450-763-2768	Sequence 2768, Ap
27	80.4	10.1	1111	10 US-10-450-763-11488	Sequence 11488, A
28	80.4	10.1	1306	3 US-09-909-650A-22	Sequence 22, Appli
29	80.4	10.1	1773	3 US-09-165-522-4	Sequence 4, Appli
30	80.4	10.1	1773	8 US-10-343-710-54	Sequence 54, Appli
31	80.4	10.1	1773	16 US-11-180-044-4	Sequence 4, Appli
32	80.4	10.1	1872	10 US-10-450-763-19249	Sequence 19249, A
33	80.4	10.1	2131	3 US-09-771-161A-87	Sequence 87, Appli
34	80.4	10.1	2155	15 US-11-127-817-12	Sequence 12, Appli
35	80.4	10.1	2372	3 US-09-165-522-6	Sequence 6, Appli
36	80.4	10.1	2372	3 US-09-165-522-7	Sequence 7, Appli
37	80.4	10.1	2372	7 US-10-305-720-1389	Sequence 1389, Ap
38	80.4	10.1	2372	10 US-10-466-162-5	Sequence 5, Appli
39	80.4	10.1	2372	10 US-10-723-681-9	Sequence 9, Appli
40	80.4	10.1	2372	10 US-10-857-780-11	Sequence 11, Appli
41	80.4	10.1	2372	15 US-11-127-817-9	Sequence 9, Appli
42	80.4	10.1	2372	16 US-11-180-044-6	Sequence 6, Appli
43	80.4	10.1	2372	16 US-11-180-044-7	Sequence 7, Appli
44	80.4	10.1	2382	10 US-10-765-700-33	Sequence 33, Appli
45	80.4	10.1	8750	3 US-09-776-167A-8	Sequence 8, Appli
46	66.8	8.3	1975	16 US-11-136-527-4334	Sequence 4334, Ap
47	66.8	8.3	1975	8 US-09-165-522-9	Sequence 9, Appli
48	66.8	8.3	1975	8 US-10-343-710-60	Sequence 60, Appli
49	66.8	8.3	1975	16 US-11-180-044-9	Sequence 9, Appli
50	66.8	8.3	1980	16 US-11-136-527-238	Sequence 238, App
51	64.4	8.1	2322	3 US-10-343-710-58	Sequence 58, Appli
52	64.4	8.1	2322	16 US-11-180-044-11	Sequence 11, Appli
53	64.4	8.1	2322	16 US-11-136-527-4293	Sequence 4293, Ap
54	50.8	6.3	600	16 US-11-136-527-197	Sequence 197, App
55	50.8	6.3	1408	16 US-11-136-527-197	Sequence 104, App
56	49.4	6.2	580	8 US-10-404-460-104	Sequence 357307,
57	49.4	6.2	520	4 US-09-925-065A-357307	Sequence 357307,
58	49.2	6.2	520	5 US-09-925-065A-357307	Sequence 357307,
59	49.2	6.2	535	12 US-10-301-480-128623	Sequence 104203,
60	49.2	6.2	535	12 US-10-301-480-1042032	Sequence 1930, Ap
61	48.8	6.1	2372	7 US-10-104-041-1930	Sequence 1930, Ap
62	48.8	6.1	2372	16 US-11-072-512-1930	Sequence 21042, A
63	48.4	6.0	450	8 US-10-242-532A-21042	Sequence 21042, A
64	48.4	6.0	450	8 US-10-085-783A-21042	Sequence 3619, Ap
65	48.4	6.0	600	13 US-11-060-756-3619	Sequence 3619, Ap
66	48.4	6.0	600	13 US-11-060-756-3620	Sequence 7891, Ap
67	48.4	6.0	600	13 US-11-060-756-7891	Sequence 7892, Ap
68	48.4	6.0	1780	3 US-09-861-097-17	Sequence 17, Appli
69	48.4	6.0	1780	3 US-09-861-098-17	Sequence 17, Appli
70	48.4	6.0	1780	3 US-09-861-012-17	Sequence 17, Appli
71	48.4	6.0	1780	10 US-10-972-052-17	Sequence 17, Appli
72	48.4	6.0	1782	7 US-10-204-041-11	Sequence 11, Appli
73	48.4	6.0	1782	8 US-10-345-444B-167	Sequence 167, App
74	48.4	6.0	1782	13 US-11-019-829-74	Sequence 74, Appli
75	48.4	6.0	1930	13 US-11-019-829-74	Sequence 74, Appli
76	48.4	6.0	36000	10 US-10-948-974A-27	Sequence 27, Appli
77	48.4	6.0	520	4 US-09-925-065A-357306	Sequence 357306,
78	48.4	6.0	520	4 US-09-925-065A-357308	Sequence 357308,
79	48.4	6.0	520	5 US-09-925-065A-357306	Sequence 357306,
80	48.4	6.0	520	5 US-09-925-065A-357308	Sequence 357308,
81	48.4	6.0	520	5 US-09-925-065A-357306	Sequence 357306,
82	48.4	6.0	535	12 US-10-301-480-128622	Sequence 428622,
83	48.4	6.0	535	12 US-10-301-480-128624	Sequence 428624,
84	48.4	6.0	535	12 US-10-301-480-1042031	Sequence 1042031,
85	48.4	6.0	535	12 US-10-301-480-1042033	Sequence 1042033,
86	46.8	5.8	1392	8 US-10-641-643-953	Sequence 953, App
87	46.8	5.8	1392	10 US-10-466-162-8	Sequence 9, Appli
88	46.8	5.8	1873	3 US-09-954-531-155	Sequence 155, App
89	46.8	5.8	1873	7 US-10-305-720-1437	Sequence 1437, Ap
90	46.8	5.8	1873	10 US-10-843-641A-1222	Sequence 1222, Ap

C 91 46.8 5.8 1873 10 US-10-872-645-12 Sequence 12, Appl
C 92 46.8 5.8 1940 13 US-11-019-823-75 Sequence 75, Appl
C 93 46.8 5.8 1940 13 US-11-019-823-76 Sequence 76, Appl
C 94 45.6 5.7 404 4 US-09-925-065A-758673 Sequence 758673,
C 95 45.6 5.7 404 5 US-09-925-065A-758673 Sequence 758673,
C 96 45.6 5.7 5986 8 US-10-321-613-396 Sequence 396, App
C 97 44.4 5.5 404 4 US-09-925-065A-758672 Sequence 758672,
C 98 44.4 5.5 404 5 US-09-925-065A-758672 Sequence 758672,
C 99 44.4 5.5 600 13 US-11-060-756-376 Sequence 376, App
C 100 44.4 5.5 600 13 US-11-060-756-377 Sequence 377, App

ALIGNMENTS

RESULT 1
US-10-723-681-2
; Sequence 2, Application US/10723681
; Publication No. US20050192239A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: BRADON, ANDREAS
; APPLICANT: KAMMERER, STEFAN M.
; APPLICANT: RENEKAND, RIKARD
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND
; FILE REFERENCE: SEQ-4069-CP
; CURRENT FILING DATE: 2003-11-25
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: US 60/429,136
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: US 60/490,234
; PRIOR FILING DATE: 2003-07-24
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 76500
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-681-2

Query Match 99.8%; Score 798.4; DB 10; Length 76500;
Best Local Similarity 99.9%; Pred. No. 2.2e-178;
Matches 799; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACATTTTCTAAACTCTTTATAGTAGAGCATAGTCTTAAAGAAAAATATATTAGCATT 60
DB 36001 ACATTTTCTAAACTCTTTATAGTAGAGCATAGTCTTAAAGAAAAATATATTAGCATT 36060

QY 61 AATTAAGTAATTTGCTCAAGTCACTAAGCAATTAAGCATTAGAGTCAAGTAAATATAT 120
DB 36061 AATTAAGTAATTTGCTCAAGTCACTAAGCAATTAAGCATTAGAGTCAAGTAAATATAT 36120

QY 121 ATGCACAAATTTGATTAATTTCTGAGTCAAGCAAGCAAAATTTTCAAGTCACTT 180
DB 36121 ATGCACAAATTTGATTAATTTCTGAGTCAAGCAAGCAAAATTTTCAAGTCACTT 36180

QY 181 AACCGAGCCCATCTTGTAGATGTTCAACTATTGTCACTCAACCTTGAGAGAGTTC 240
DB 36181 AACCGAGCCCATCTTGTAGATGTTCAACTATTGTCACTCAACCTTGAGAGAGTTC 36240

QY 241 AAACACTAAGATGAATGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
DB 36241 AAACACTAAGATGAATGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 36300

QY 301 GACTGATGATCAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB 36301 GACTGATGATCAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 36360

QY 361 GCCCATGTTACATTTTCTTCAAGATTCATTAATTAATTAATTAATTAATTAATTAATTAAT 420
DB 36361 GCCCATGTTACATTTTCTTCAAGATTCATTAATTAATTAATTAATTAATTAATTAATTAAT 36420

QY 421 TGTCTGATCATTAACATCAGATATATATGACACTGAATATCAAAAAGA 480
DB 36421 TGTCTGATCATTAACATCAGATATATATGACACTGAATATCAAAAAGA 36480

QY 481 ATAAAGCTAAATCTTTTAAAGGACCAACATGATATTTGTCATGCTGCTTAAAG 540
DB 36481 ATAAAGCTAAATCTTTTAAAGGACCAACATGATATTTGTCATGCTGCTTAAAG 36540

QY 541 CAATGTTATGTTATTTCTGCAACCCCTACACAAAGGCCAAGAAATTAACAAGTACTAG 600
DB 36541 CAATGTTATGTTATTTCTGCAACCCCTACACAAAGGCCAAGAAATTAACAAGTACTAG 36600

QY 601 TTTATTTGTTATTCACGAGAGTGTGATCTTAAGAGAGAGGCTGCTTTTACTACAC 660
DB 36601 TTTATTTGTTATTCACGAGAGTGTGATCTTAAGAGAGAGGCTGCTTTTACTACAC 36660

QY 661 ATTTTATGCTTTTCTTCTGAAATCATTAATCTTCTTGTAGATTAATTTCTGTAAGAACG 720
DB 36661 ATTTTATGCTTTTCTTCTGAAATCATTAATCTTCTTGTAGATTAATTTCTGTAAGAACG 36720

QY 721 CTGCTTATTAATAGAAAACAATTTATCTTATCCACAGGAAATTCATTAATTC 780
DB 36721 CTGCTTATTAATAGAAAACAATTTATCTTATCCACAGGAAATTCATTAATTC 36780

QY 781 CAATTAATTAAGCTTTGATG 800
DB 36781 CAATTAATTAAGCTTTGATG 36800

RESULT 2
US-10-857-780-2
; Sequence 2, Application US/10857780
; Publication No. US20050272043A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: BRAUN, ANDREAS
; APPLICANT: KAMMERER, STEFAN M.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: RENEKAND, RIKARD HENRY
; APPLICANT: HOVAL-WRIGHTSON, CAROLYN R.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
; FILE REFERENCE: SEQ-4069-CP
; CURRENT FILING DATE: 2004-05-28
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 10/723,681
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/490,234
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: 60/525,239
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 4962
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 110950
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-857-780-2

Query Match 99.8%; Score 798.4; DB 10; Length 110950;
Best Local Similarity 99.9%; Pred. No. 2.6e-178;
Matches 799; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACATTTTCTAAACTCTTTATAGTAGAGCATAGTCTTAAAGAAAAATATATTAGCATT 60
DB 36016 ACATTTTCTAAACTCTTTATAGTAGAGCATAGTCTTAAAGAAAAATATATTAGCATT 36075

QY 61 AATTAAGTAATTTGCTCAAGTCACTAAGCAATTAAGCATTAGAGTCAAGTAAATATAT 120
DB 36076 AATTAAGTAATTTGCTCAAGTCACTAAGCAATTAAGCATTAGAGTCAAGTAAATATAT 36135

QY 121 ATGCACAAATTTGATTAATTTCTGAGTCAAGCAAGCAAAATTTTCAAGTCACTT 180

```
Db 36136 ATGACAAATTGTGATTAGATTCTGTGCTAGCAAGAAAATTTTCCAAAGCTGACCTT 36195
QY 181 AACCGGAGCCCATTTGGTAGATGTTTCAATATTGTCACATCAACCTTGAGAAAGATTC 240
Db 36196 AACCGGAGCCCATTTGGTAGATGTTTCAATATTGTCACATCAACCTTGAGAAAGATTC 36255
QY 241 AAACACTAAGATGAATGAGGAGAGAGTAGCGGCTGAAAAGATTACTGAGCTCCACATT 300
Db 36256 AAACACTAAGATGAATGAGGAGAGAGTAGCGGCTGAAAAGATTACTGAGCTCCACATT 36315
QY 301 GACTTGATGTCAAAAGGCAATTATGCTCTGTAATTTTGATGAGGCACTTTACCCCTTA 360
Db 36316 GACTTGATGTCAAAAGGCAATTATGCTCTGTAATTTTGATGAGGCACTTTACCCCTTA 36375
QY 361 GCCCATGTTAACTTTTCTTCAGGATTCATTACTATTAAATTTATTTATGAAAAAGTTT 420
Db 36376 GCCCATGTTAACTTTTCTTCAGGATTCATTACTATTAAATTTATTTATGAAAAAGTTT 36435
QY 421 TGTCTGATCATTTACATGAGAAATATGCAATGAAATGCGACACTGAAATATCAAAAGAA 480
Db 36436 TGTCTGATCATTTACATGAGAAATATGCAATGAAATGCGACACTGAAATATCAAAAGAA 36495
QY 481 ATAAACTAAATCATTTATAGACACAAACCATGATATTTGTCATCTGCTCTTTAG 540
Db 36496 ATAAACTAAATCATTTATAGACACACAAACCATGATATTTGTCATCTGCTCTTTAG 36555
QY 541 CAATGTTATGTTATTTCTTGCAACCCCTACACAAAGGCCAAGAAATTACAAAGTACTAG 600
Db 36556 CAATGTTATGTTATTTCTTGCAACCCCTACACAAAGGCCAAGAAATTACAAAGTACTAG 36615
QY 601 TTATATGTTATTCAGGAGAGTAGAGTACTGAAAGAGAGAGGCTGCTCTTTACTACAC 660
Db 36616 TTATATGTTATTCAGGAGAGTAGAGTACTGAAAGAGAGAGGCTGCTCTTTACTACAC 36675
QY 661 ATTTTAGCTTTTCTTCTGAAATTCATTACTCTCTTGATAGATTAAGTTCTGTAGAAACAG 720
Db 36676 ATTTTAGCTTTTCTTCTGAAATTCATTACTCTCTTGATAGATTAAGTTCTGTAGAAACAG 36735
QY 721 CTGTGTTATTTATGAAAACAAAATTTATCCTTCATCCACAGGGAATTCATTACTTAATGC 780
Db 36736 CTGTGTTATTTATGAAAACAAAATTTATCCTTCATCCACAGGGAATTCATTACTTAATGC 36795
QY 781 CAATAATTTAGCTTTTGATG 800
Db 36796 CAATAATTTAGCTTTTGATG 36815

RESULT 3
US-09-925-065A-683710/c
; Sequence 683710, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243, 096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252, 147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250, 092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261, 766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289, 846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 683710
; LENGTH: 2669
```

```
TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-683710
Query Match 99.6%; Score 796.8; DB 4; Length 2669;
Best Local Similarity 99.8%; Pred. No. 1,2e-178;
Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACATTTTCTAAAACCTTTTATAGTAGAGCATGCTTTAGAAAAAATATATTAGCATTT 60
Db 1478 ACATTTTCTAAAACCTTTTATAGTAGAGCATGCTTTAGAAAAAATATATTAGCATTT 1419
QY 61 AATAAGTAATGTCTCAAGTCACTAATAAGCACTTACTAGGATGAGTAAATAATAT 120
Db 1418 AATAAGTAATGTCTCAAGTCACTAATAAGCACTTACTAGGATGAGTAAATAATATAT 1359
QY 121 ATGCACAATTGTGATTTAGATTCTGTGCTAGCAAAAGAAAAATTTTCCAGCTGACCTT 180
Db 1358 ATGCACAATTGTGATTTAGATTCTGTGCTAGCAAAAGAAAAATTTTCCAGCTGACCTT 1299
QY 181 AACCGAGCCCATCTTGATAGATGTTTCACTATTGTCACTCAACCTTGAGAGAGTTT 240
Db 1298 AACCGAGCCCATCTTGATAGATGTTTCACTATTGTCACTCAACCTTGAGAGAGTTT 1239
QY 241 AAACACTAAGATGAATGAGGAGAGTAGCGGCTGAAAAGATTACTGAGCTCCACATT 300
Db 1238 AAACACTAAGATGAATGAGGAGAGTAGCGGCTGAAAAGATTACTGAGCTCCACATT 1179
QY 301 GACTTGATGTCAAAAGGCAATTATGCTCTGTAATTTTGATGAGGCACTTTACCCCTTA 360
Db 1178 GACTTGATGTCAAAAGGCAATTATGCTCTGTAATTTTGATGAGGCACTTTACCCCTTA 1119
QY 361 GCCCATGTTAACTTTTCTTCAGGATTCATTACTATTAAATTTATTTATGAAAAAGTTT 420
Db 1118 GCCCATGTTAACTTTTCTTCAGGATTCATTACTATTAAATTTATTTATGAAAAAGTTT 1059
QY 421 TGTCTGATCATTTACATGAGAAATATGCAATGAAATGCGACACTGAAATATCAAAAGAA 480
Db 1058 TGTCTGATCATTTACATGAGAAATATGCAATGAAATGCGACACTGAAATATCAAAAGAA 999
QY 481 ATAAACTAAATCATTTATAGACACAAACCATGATATTTGTCATCTGCTCTTTAG 540
Db 998 ATAAACTAAATCATTTATAGACACAAACCATGATATTTGTCATCTGCTCTTTAG 939
QY 541 CAATGTTATGTTATTTCTTGCAACCCCTACACAAAGGCCAAGAAATTACAAAGTACTAG 600
Db 938 CAATGTTATGTTATTTCTTGCAACCCCTACACAAAGGCCAAGAAATTACAAAGTACTAG 879
QY 601 TTATATGTTATTCAGGAGAGTAGAGTACTGAAAGAGAGGCTGCTTTACTACAC 660
Db 878 TTATATGTTATTCAGGAGAGTAGAGTACTGAAAGAGAGGCTGCTTTACTACAC 819
QY 661 ATTTTAGCTTTTCTTCTGAAATTCATTACTCTCTTGATAGATTAAGTTCTGTAGAAACAG 720
Db 818 ATTTTAGCTTTTCTTCTGAAATTCATTACTCTCTTGATAGATTAAGTTCTGTAGAAACAG 759
QY 721 CTGTGTTATTTATGAAAACAAAATTTATCCTTCATCCACAGGGAATTCATTACTTAATGC 780
Db 758 CTGTGTTATTTATGAAAACAAAATTTATCCTTCATCCACAGGGAATTCATTACTTAATGC 699
QY 781 CAATAATTTAGCTTTTGATG 800
Db 698 CAATAATTTAGCTTTTGATG 679

RESULT 4
US-09-925-065A-683711/c
; Sequence 683711, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
```

```
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925, 065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243, 096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252, 147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250, 092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261, 766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289, 846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 683711
LENGTH: 2669
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-683711
```

Query Match 99.6%; Score 796.8; DB 4; Length 2669;

Best Local Similarity 99.8%; Pred. No. 1.2e-178;

Matches 798; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 ACATTTCTTAAACCTTTTATAGTGAAGCATGCTCTTGAAGAAAAATATATAGCATT 60
DB 1478 ACATTTCTTAAACCTTTTATAGTGAAGCATGCTCTTGAAGAAAAATATATAGCATT 1419
QY 61 AATAAGTAATGTCTCAGTCACTACTAAAGCATTACTAGATCAGTAAATAATAT 120
DB 1418 AATAAGTAATGTCTCAGTCACTACTAAAGCATTACTAGATCAGTAAATAATAT 1359
QY 121 ATGCAAAATGTGTATAGATTCTGTGCTAGCAACGAAAAATTTCCAGCTGACCTT 180
DB 1358 ATGCAAAATGTGTATAGATTCTGTGCTAGCAACGAAAAATTTCCAGCTGACCTT 1299
QY 181 AACCGAGCCCATCTTGTATGATGTTTCACTATTTGTCACTAACCTTGAGAGATTTC 240
DB 1298 AACCGAGCCCATCTTGTATGATGTTTCACTATTTGTCACTAACCTTGAGAGATTTC 1239
QY 241 AAACCTAAGATGAATGAGGAGAGAGTGAAGGCTGAAAGATTCTGAGCTCCACATT 300
DB 1238 AAACCTAAGATGAATGAGGAGAGAGTGAAGGCTGAAAGATTCTGAGCTCCACATT 1179
QY 301 GACTTGATGCTCAAAAGGCAATTATGCTCTGAATTTTGAAGGACATTTACCTTTA 360
DB 1178 GACTTGATGCTCAAAAGGCAATTATGCTCTGAATTTTGAAGGACATTTACCTTTA 1119
QY 361 GCCCATGTTAACTTTTCTTCAAGATTCACTACTATTTAAATTTATTTAAGAAAAAGTTT 420
DB 1118 GCCCATGTTAACTTTTCTTCAAGATTCACTACTATTTAAATTTATTTAAGAAAAAGTTT 1059
QY 421 TGTCTGATCATTTACCATCAGAAATATGAAATGAAATGCACTGAATATCAAAAGAA 480
DB 1058 TGTCTGATCATTTACCATCAGAAATATGAAATGAAATGCACTGAATATCAAAAGAA 999
QY 481 ATAAAACTAAATCACTATTAAGGACAAACCATGTATATTTGTCCATGTGCTCTTTAAG 540
DB 998 ATAAAACTAAATCACTATTAAGGACAAACCATGTATATTTGTCCATGTGCTCTTTAAG 939
QY 541 CAATGTATATTTATTTCTTCAACCCCTTACACAAAGCCCAAGAAATTAACAAGTACTAG 600
DB 938 CAATGTATATTTATTTCTTCAACCCCTTACACAAAGCCCAAGAAATTAACAAGTACTAG 879
QY 601 TTTATGTTATTCACGAGAGTGAAGTACTGAAGAGAGAGGCTGCTTTTACTACAC 660
DB 878 TTTATGTTATTCACGAGAGTGAAGTACTGAAGAGAGAGGCTGCTTTTACTACAC 819
QY 661 ATTTTATGCTTTTCTTCTGAAATTCATCTTCTTGAAGATTAAGTTCTGAAGAAACAG 720
DB 818 ATTTTATGCTTTTCTTCTGAAATTCATCTTCTTGAAGATTAAGTTCTGAAGAAACAG 759
```

```
QY 721 CTGTGTATATAGAAAAAACAATTTATCTTCATCCACAGGGAATTTACTTAATGC 780
DB 758 CTGTGTATATATAGAAAAAACAATTTATCTTCATCCACAGGGAATTTACTTAATGC 699
QY 781 CAATATATAGTTTGTATG 800
DB 698 CAATATATAGTTTGTATG 679
```

RESULT 5

US-09-925-065A-683712/c

Sequence 683712, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925, 065A

NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 683712

LENGTH: 2669

TYPE: DNA

ORGANISM: Homo sapiens

US-09-925-065A-683712

Query Match 99.6%; Score 796.8; DB 4; Length 2669;

Best Local Similarity 99.8%; Pred. No. 1.2e-178;

Matches 798; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 ACATTTCTTAAACCTTTTATAGTGAAGCATGCTCTTGAAGAAAAATATATAGCATT 60
DB 1478 ACATTTCTTAAACCTTTTATAGTGAAGCATGCTCTTGAAGAAAAATATATAGCATT 1419
QY 61 AATAAGTAATGTCTCAGTCACTACTAAAGCATTACTAGATCAGTAAATAATAT 120
DB 1418 AATAAGTAATGTCTCAGTCACTACTAAAGCATTACTAGATCAGTAAATAATAT 1359
QY 121 ATGCAAAATGTGTATAGATTCTGTGCTAGCAACGAAAAATTTCCAGCTGACCTT 180
DB 1358 ATGCAAAATGTGTATAGATTCTGTGCTAGCAACGAAAAATTTCCAGCTGACCTT 1299
QY 181 AACCGAGCCCATCTTGTATGATGTTTCACTATTTGTCACTAACCTTGAGAGATTTC 240
DB 1298 AACCGAGCCCATCTTGTATGATGTTTCACTATTTGTCACTAACCTTGAGAGATTTC 1239
QY 241 AAACCTAAGATGAATGAGGAGAGAGTGAAGGCTGAAAGATTCTGAGCTCCACATT 300
DB 1238 AAACCTAAGATGAATGAGGAGAGAGTGAAGGCTGAAAGATTCTGAGCTCCACATT 1179
QY 301 GACTTGATGCTCAAAAGGCAATTATGCTCTGAATTTTGAAGGACATTTACCTTTA 360
DB 1178 GACTTGATGCTCAAAAGGCAATTATGCTCTGAATTTTGAAGGACATTTACCTTTA 1119
QY 361 GCCCATGTTAACTTTTCTTCAAGATTCACTACTATTTAAATTTATTTAAGAAAAAGTTT 420
DB 1118 GCCCATGTTAACTTTTCTTCAAGATTCACTACTATTTAAATTTATTTAAGAAAAAGTTT 1059
QY 421 TGTCTGATCATTTACCATCAGAAATATGAAATGAAATGCACTGAATATCAAAAGAA 480
DB 1058 TGTCTGATCATTTACCATCAGAAATATGAAATGAAATGCACTGAATATCAAAAGAA 999
```


Best Local Similarity 99.8%; Pred. No. 1.2e-178;
Matches 798; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 ACATTTTCTAAAACCTTTTATAGTACAGATAGTCTTGTAGAAAAATATATAGCATT 60
Db 1478 ACATTTTCTAAAACCTTTTATAGTACAGATAGTCTTGTAGAAAAATATATAGCATT 1419
QY 61 AATAAGTAATTTGCTCAAGTCTACTTAAAGCATTACTAGATCAGTAAAAATATAT 120
Db 1418 AATAAGTAATTTGCTCAAGTCTACTTAAAGCATTACTAGATCAGTAAAAATATAT 1359
QY 121 ATGCACAAATGTGTATAGATTCTGTGGCTAGCAAAAGAAAAATTTTCCAGCTGACCTT 180
Db 1358 ATGCACAAATGTGTATAGATTCTGTGGCTAGCAAAAGAAAAATTTTCCAGCTGACCTT 1299
QY 181 AACCGAGAGCCCATCTGTGTAGATGTTTCAACTATTTGCATCATCAACCTTGAGAGATTC 240
Db 1298 AACCGAGAGCCCATCTGTGTAGATGTTTCAACTATTTGCATCATCAACCTTGAGAGATTC 1239
QY 241 AATCACTAAGATGATGAGGAGAGAGTGGCGCTGAAAGATTTACTGAGCTCCACATT 300
Db 1238 AATCACTAAGATGATGAGGAGAGAGTGGCGCTGAAAGATTTACTGAGCTCCACATT 1179
QY 301 GACTTGATGCTCAAAAAGGCGATTATGGCTCTGAATTTTGTAGAGCATTACCCCTTAA 360
Db 1178 GACTTGATGCTCAAAAAGGCGATTATGGCTCTGAATTTTGTAGAGCATTACCCCTTAA 1119
QY 361 GCCCATGTTAACTTTTCTTCAAGATTCATTACTATTAATTAATTAAGAAAAAGTTT 420
Db 1118 GCCCATGTTAACTTTTCTTCAAGATTCATTACTATTAATTAATTAAGAAAAAGTTT 1059
QY 421 TGCTCGATCATTTACATGAGAAATATCGAATGAAATGCGACACCTGAATTCAAAAAGAA 480
Db 421 TGCTCGATCATTTACATGAGAAATATCGAATGAAATGCGACACCTGAATTCAAAAAGAA 999
QY 1058 TGCTCGATCATTTACATGAGAAATATCGAATGAAATGCGACACCTGAATTCAAAAAGAA 999
Db 481 ATAAACTAAATCATTTATTAAGACACAAACATGATGATTTTGTCAATCTGCTCTTAA 540
QY 998 ATAAACTAAATCATTTATTAAGACACAAACATGATGATTTTGTCAATCTGCTCTTAA 540
Db 998 ATAAACTAAATCATTTATTAAGACACAAACATGATGATTTTGTCAATCTGCTCTTAA 939
QY 541 CAATGTTATGTTATTTCTTGCAACCCCTTACACAAAGGCCCAAGAAATTAACAAGTAC 600
Db 938 CAATGTTATGTTATTTCTTGCAACCCCTTACACAAAGGCCCAAGAAATTAACAAGTAC 879
QY 601 TTTATGTTATTTCAAGGAGAGTGAATCCTGAAGGAGAGGCTGCTCTTTTACTACAC 660
Db 878 TTTATGTTATTTCAAGGAGAGTGAATCCTGAAGGAGAGGCTGCTCTTTTACTACAC 819
QY 661 ATTTTATGCTTTTCTTCTGAATTTCAATCTCTTGTAGATTAAGTTCTGTAGAAACAG 720
Db 818 ATTTTATGCTTTTCTTCTGAATTTCAATCTCTTGTAGATTAAGTTCTGTAGAAACAG 759
QY 721 CTGTGTTATTAAGAAAAAACAATTTATCTTCATCCACAGGAAATTAATTAATG 780
Db 758 CTGTGTTATTAAGAAAAAACAATTTATCTTCATCCACAGGAAATTAATTAATG 699
QY 781 CAATTAATTAACCTTTTGAATG 800
Db 698 CAATTAATTAACCTTTTGAATG 679
```

RESULT 8

US-09-925-065A-683712/c
; Sequence 683712, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243, 096
; PRIOR FILING DATE: 2000-10-24

;; PRIOR APPLICATION NUMBER: US 60/252,147
;; PRIOR FILING DATE: 2000-11-20
;; PRIOR APPLICATION NUMBER: US 60/250,092
;; PRIOR FILING DATE: 2000-11-30
;; PRIOR APPLICATION NUMBER: US 60/261,766
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: US 60/289,846
;; PRIOR FILING DATE: 2001-05-09
;; NUMBER OF SEQ ID NOS: 957086
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 683712
;; LENGTH: 2669
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-925-065A-683712

Query Match 99.6%; Score 796.8; DB 5; Length 2669;
Best Local Similarity 99.8%; Pred. No. 1.2e-178;
Matches 798; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 ACATTTTCTAAAACCTTTTATAGTACAGATAGTCTTGTAGAAAAATATATAGCATT 60
Db 1478 ACATTTTCTAAAACCTTTTATAGTACAGATAGTCTTGTAGAAAAATATATAGCATT 1419
QY 61 AATAAGTAATTTGCTCAAGTCTACTTAAAGCATTACTAGATCAGTAAAAATATAT 120
Db 1418 AATAAGTAATTTGCTCAAGTCTACTTAAAGCATTACTAGATCAGTAAAAATATAT 1359
QY 121 ATGCACAAATGTGTATAGATTCTGTGGCTAGCAAAAGAAAAATTTTCCAGCTGACCTT 180
Db 1178 ATGCACAAATGTGTATAGATTCTGTGGCTAGCAAAAGAAAAATTTTCCAGCTGACCTT 1299
QY 181 AACCGAGAGCCCATCTGTGTAGATGTTTCAACTATTTGCATCATCAACCTTGAGAGATTC 240
Db 1298 AACCGAGAGCCCATCTGTGTAGATGTTTCAACTATTTGCATCATCAACCTTGAGAGATTC 1239
QY 241 AATCACTAAGATGATGAGGAGAGAGTGGCGCTGAAAGATTTACTGAGCTCCACATT 300
Db 1238 AATCACTAAGATGATGAGGAGAGAGTGGCGCTGAAAGATTTACTGAGCTCCACATT 1179
QY 301 GACTTGATGCTCAAAAAGGCGATTATGGCTCTGAATTTTGTAGAGCATTACCCCTTAA 360
Db 1178 GACTTGATGCTCAAAAAGGCGATTATGGCTCTGAATTTTGTAGAGCATTACCCCTTAA 1119
QY 361 GCCCATGTTAACTTTTCTTCAAGATTCATTACTATTAATTAATTAAGAAAAAGTTT 420
Db 1118 GCCCATGTTAACTTTTCTTCAAGATTCATTACTATTAATTAATTAAGAAAAAGTTT 1059
QY 421 TGCTCGATCATTTACATGAGAAATATCGAATGAAATGCGACACCTGAATTCAAAAAGAA 480
Db 1058 TGCTCGATCATTTACATGAGAAATATCGAATGAAATGCGACACCTGAATTCAAAAAGAA 999
QY 481 ATAAACTAAATCATTTATTAAGACACAAACATGATGATTTTGTCAATCTGCTCTTAA 540
Db 998 ATAAACTAAATCATTTATTAAGACACAAACATGATGATTTTGTCAATCTGCTCTTAA 939
QY 541 CAATGTTATGTTATTTCTTGCAACCCCTTACACAAAGGCCCAAGAAATTAACAAGTAC 600
Db 938 CAATGTTATGTTATTTCTTGCAACCCCTTACACAAAGGCCCAAGAAATTAACAAGTAC 879
QY 601 TTTATGTTATTTCAAGGAGAGTGAATCCTGAAGGAGAGGCTGCTCTTTTACTACACC 660
Db 878 TTTATGTTATTTCAAGGAGAGTGAATCCTGAAGGAGAGGCTGCTCTTTTACTACACC 819
QY 661 ATTTTATGCTTTTCTTCTGAATTTCAATCTCTTGTAGATTAAGTTCTGTAGAAACAG 720
Db 818 ATTTTATGCTTTTCTTCTGAATTTCAATCTCTTGTAGATTAAGTTCTGTAGAAACAG 759
QY 721 CTGTGTTATTAAGAAAAAACAATTTATCTTCATCCACAGGAAATTAATTAATG 780
Db 758 CTGTGTTATTAAGAAAAAACAATTTATCTTCATCCACAGGAAATTAATTAATG 699
QY 781 CAATTAATTAACCTTTTGAATG 800
```


Db 698 CAAATATTAAGTTTATG 679

RESULT 9

US-10-857-780-4942
; Sequence 4942, Application US/10857780
; Publication No. US20050272043A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: BRAUN, ANDREAS
; APPLICANT: KAMERER, STEFAN M.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: REMELAND, RIKARD HENRY
; APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
; FILE REFERENCE: SEQ-4069-CP
; CURRENT APPLICATION NUMBER: US/10/857,780
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 10/723,681
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/490,234
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: 60/525,239
; NUMBER OF SEQ ID NOS: 4962
; SOFTWARE: PatentIn version 3.2
; LENGTH: 823
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-857-780-4942

Query Match 57.9%; Score 463.4; DB 10; Length 823;
Best Local Similarity 99.8%; Pred. No. 1.3e-99;
Matches 464; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 336 TTTGATGAGGCACATTTACCCCTTTAGCCCATGTTAACTTTCTTCAGATTCTATTACTA 395
| 1 TTTGATGAGGCACATTTACCCCTTTAGCCCATGTTAACTTTCTTCAGATTCTATTACTA 60
| 396 TTTAAATATTATGAAAAAGTTTGTCTGATCATTCACATCAGAAATATCAGATG 455
| 61 TTTAAATATTATGAAAAAGTTTGTCTGATCATTCACATCAGAAATATCAGATG 120
| 456 AATGCCACACTGAATATCAAAAGAAATAACTAAATCATTTAAGACACACCATGT 515
| 121 AATGCCACACTGAATATCAAAAGAAATAACTAAATCATTTAAGACACACCATGT 180
| 516 GATATTGTCCATCTGCTCTTTAAGCAATGTTATGTTATTTCTGCAACCCCTACACAA 575
| 181 GATATTGTCCATCTGCTCTTTAAGCAATGTTATGTTATTTCTGCAACCCCTACACAA 240
| 576 GGCAGAAATATACAGAGTACTAGTTTATGTTATTCGAGAGTGTAGTACCTGAAG 635
| 241 GGCAGAAATATACAGAGTACTAGTTTATGTTATTCGAGAGTGTAGTACCTGAAG 300
| 636 GAGAAAGCTGTCTTTTACTACACATTTTATGCTTTTCTTCTGAATTCATTCTCT 695
| 301 GAGAAAGCTGTCTTTTACTACACATTTTATGCTTTTCTTCTGAATTCATTCTCT 360
| 696 TGTATGTAAGTTCTGTGAAGAAACAGCTGTGTATTTAAGAAAACAAAATTTATCTTCATC 755
| 361 TGTATGTAAGTTCTGTGAAGAAACAGCTGTGTATTTAAGAAAACAAAATTTATCTTCATC 420
| 756 CACAGGAAATTCATTACTTAATGCAAAATTAATGCTTTTGATG 800
| 421 CACAGGAAATTCATTACTTAATGCAAAATTAATGCTTTTGATG 465

RESULT 10
US-10-857-780-4943

; Sequence 4943, Application US/10857780
; Publication No. US20050272043A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: BRAUN, ANDREAS
; APPLICANT: KAMERER, STEFAN M.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: REMELAND, RIKARD HENRY
; APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
; FILE REFERENCE: SEQ-4069-CP
; CURRENT APPLICATION NUMBER: US/10/857,780
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 10/723,681
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/490,234
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: 60/525,239
; NUMBER OF SEQ ID NOS: 4962
; SOFTWARE: PatentIn version 3.2
; LENGTH: 823
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-857-780-4943

Query Match 57.9%; Score 463.4; DB 10; Length 823;
Best Local Similarity 99.8%; Pred. No. 1.3e-99;
Matches 464; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 336 TTTGATGAGGCACATTTACCCCTTTAGCCCATGTTAACTTTCTTCAGATTCTATTACTA 395
| 1 TTTGATGAGGCACATTTACCCCTTTAGCCCATGTTAACTTTCTTCAGATTCTATTACTA 60
| 396 TTTAAATATTATGAAAAAGTTTGTCTGATCATTCACATCAGAAATATCAGATG 455
| 61 TTTAAATATTATGAAAAAGTTTGTCTGATCATTCACATCAGAAATATCAGATG 120
| 456 AATGCCACACTGAATATCAAAAGAAATAACTAAATCATTTAAGACACACCATGT 515
| 121 AATGCCACACTGAATATCAAAAGAAATAACTAAATCATTTAAGACACACCATGT 180
| 516 GATATTGTCCATCTGCTCTTTAAGCAATGTTATGTTATTTCTGCAACCCCTACACAA 575
| 181 GATATTGTCCATCTGCTCTTTAAGCAATGTTATGTTATTTCTGCAACCCCTACACAA 240
| 576 GGCAGAAATATACAGAGTACTAGTTTATGTTATTCGAGAGTGTAGTACCTGAAG 635
| 241 GGCAGAAATATACAGAGTACTAGTTTATGTTATTCGAGAGTGTAGTACCTGAAG 300
| 636 GAGAAAGCTGTCTTTTACTACACATTTTATGCTTTTCTTCTGAATTCATTCTCT 695
| 301 GAGAAAGCTGTCTTTTACTACACATTTTATGCTTTTCTTCTGAATTCATTCTCT 360
| 696 TGTATGTAAGTTCTGTGAAGAAACAGCTGTGTATTTAAGAAAACAAAATTTATCTTCATC 755
| 361 TGTATGTAAGTTCTGTGAAGAAACAGCTGTGTATTTAAGAAAACAAAATTTATCTTCATC 420
| 756 CACAGGAAATTCATTACTTAATGCAAAATTAATGCTTTTGATG 800
| 421 CACAGGAAATTCATTACTTAATGCAAAATTAATGCTTTTGATG 465

RESULT 11
US-09-925-065A-44644/c
; Sequence 44644, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome

```
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925, 065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243, 096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252, 147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250, 092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261, 766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289, 846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 44644
LENGTH: 572
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-44644

Query Match
Best Local Similarity 57.0%; Score 456.4; DB 4; Length 572;
Pred. No. 5.3e-98;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

343 AGGCACATTACCCCTTTAGCCCATGTTACATTTCTTCAGATTCATTAATAAT 402
572 AGGCACATTACCCCTTTAGCCCATGTTACATTTCTTCAGATTCATTAATAAT 513
403 TATTTATGAAAAAGTTTGTCTGATCATTAACATTAATAGAAATGCA 462
512 TATTTATGAAAAAGTTTGTCTGATCATTAACATTAATAGAAATGCA 453
463 CACTGAATATCAAAAGAAATAAATACTAAATCATTAATAGACACACATGTATTT 522
452 CACTGAATATCAAAAGAAATAAATACTAAATCATTAATAGACACACATGTATTT 393
523 GTTCATCTGCTCTTTAAGCAATGTATTTCTTGCAACCCCTACACAAAGCCAAAG 582
392 GTTCATCTGCTCTTTAAGCAATGTATTTCTTGCAACCCCTACACAAAGCCAAAG 333
583 AAATTCACAGAGTACTGTTATGTTATTCAGAGAGTACTGTTATGAGAGAGG 642
332 AAATTCACAGAGTACTGTTATGTTATTCAGAGAGTACTGTTATGAGAGG 273
643 CTGTCCTTTACTACACATTTTAACTTTCTTCTGATTCATTAATCTTGTAGAT 702
272 CTGTCCTTTACTACACATTTTAACTTTCTTCTGATTCATTAATCTTGTAGAT 213
703 AAGTTCGTAGAAACAGCTGTGTATATATGAAAAAAATTAATCTTGTAGAT 762
212 AAGTTCGTAGAAACAGCTGTGTATATATGAAAAAAATTAATCTTGTAGAT 153
763 AAATTCATTAATGAGCAATTAATTAATGAGTGTAGAT 800
152 AAATTCATTAATGAGCAATTAATTAATGAGTGTAGAT 115

RESULT 12
US-09-925-065A-44644/c
Sequence 44644, Application US/09925065A
Publication No. US2005028172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925, 065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243, 096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252, 147
PRIOR FILING DATE: 2000-11-20
```

```

PRIOR APPLICATION NUMBER: US 60/250, 092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261, 766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289, 846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 44644
LENGTH: 572
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-44644

Query Match
Best Local Similarity 57.0%; Score 456.4; DB 5; Length 572;
Pred. No. 5.3e-98;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

343 AGGCACATTACCCCTTTAGCCCATGTTACATTTCTTCAGATTCATTAATAAT 402
572 AGGCACATTACCCCTTTAGCCCATGTTACATTTCTTCAGATTCATTAATAAT 513
403 TATTTATGAAAAAGTTTGTCTGATCATTAACATTAATAGAAATGCA 462
512 TATTTATGAAAAAGTTTGTCTGATCATTAACATTAATAGAAATGCA 453
463 CACTGAATATCAAAAGAAATAAATACTAAATCATTAATAGACACACATGTATTT 522
452 CACTGAATATCAAAAGAAATAAATACTAAATCATTAATAGACACACATGTATTT 393
523 GTTCATCTGCTCTTTAAGCAATGTATTTCTTGCAACCCCTACACAAAGCCAAAG 582
392 GTTCATCTGCTCTTTAAGCAATGTATTTCTTGCAACCCCTACACAAAGCCAAAG 333
583 AAATTCACAGAGTACTGTTATGTTATTCAGAGAGTACTGTTATGAGAGAGG 642
332 AAATTCACAGAGTACTGTTATGTTATTCAGAGAGTACTGTTATGAGAGG 273
643 CTGTCCTTTACTACACATTTTAACTTTCTTCTGATTCATTAATCTTGTAGAT 702
272 CTGTCCTTTACTACACATTTTAACTTTCTTCTGATTCATTAATCTTGTAGAT 213
703 AAGTTCGTAGAAACAGCTGTGTATATATGAAAAAAATTAATCTTGTAGAT 762
212 AAGTTCGTAGAAACAGCTGTGTATATATGAAAAAAATTAATCTTGTAGAT 153
763 AAATTCATTAATGAGCAATTAATTAATGAGTGTAGAT 800
152 AAATTCATTAATGAGCAATTAATTAATGAGTGTAGAT 115

RESULT 13
US-10-301-480-145882/c
Sequence 145882, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301, 480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215, 598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311, 695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 145882
LENGTH: 572
TYPE: DNA
ORGANISM: Homo sapiens
US-10-301-480-145882
```

Query Match 57.0%; Score 456.4; DB 12; Length 572;
Best Local Similarity 99.8%; Pred. No. 5.3e-98;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 343 AGGCAATTACCTTTAGCCAGTGTAACTTTCTCAGATTCTTAAAT 402
DB 572 AGGCAATTACCTTTAGCCAGTGTAACTTTCTCAGATTCTTAAAT 513
QY 403 TATTATGAAAAAGTTTGTCTGATCACTTACATCAATATCAAGATGCA 462
DB 512 TATTATGAAAAAGTTTGTCTGATCACTTACATCAATATCAAGATGCA 453
QY 463 CACTGAATATCAAAAGAAATTAATCTAATTAAGACACAAACCTGATATT 522
DB 452 CACTGAATATCAAAAGAAATTAATCTAATTAAGACACAAACCTGATATT 393
QY 523 GTCCATCTGCTCTTTAAGCAATGTATTTCTTGCAACCCCTACACAAAGCCAG 582
DB 392 GTCCATCTGCTCTTTAAGCAATGTATTTCTTGCAACCCCTACACAAAGCCAG 333
QY 583 AAATTACACAAGTACTAGTTTATGTTATTCACGAGAGTGAATCTGAAGAGAAG 642
DB 332 AAATTACACAAGTACTAGTTTATGTTATTCACGAGAGTGAATCTGAAGAGAAG 273
QY 643 CTGTCTTTTACTACACCAATTTTACTCTTTCTTGCAATTAATCTTCTGTAGAT 702
DB 272 CTGTCTTTTACTACACCAATTTTACTCTTTCTTGCAATTAATCTTCTGTAGAT 213
QY 703 AAGTCTGTAGAAAACAGCTGTGTATTTATAGAAAACAAATTTATCTTCATCACAAGG 762
DB 212 AAGTCTGTAGAAAACAGCTGTGTATTTATAGAAAACAAATTTATCTTCATCACAAGG 153
QY 763 AAATTCATTACTTAATGCCAAATTAATACGTTTGATG 800
DB 152 AAATTCATTACTTAATGCCAAATTAATACGTTTGATG 115

RESULT 14

US-10-301-480-759291/c
; Sequence 759291, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 759291
; LENGTH: 572
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-759291

Query Match 57.0%; Score 456.4; DB 12; Length 572;

Best Local Similarity 99.8%; Pred. No. 5.3e-98;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 343 AGGCAATTACCTTTAGCCAGTGTAACTTTCTCAGATTCTTAAAT 402
DB 572 AGGCAATTACCTTTAGCCAGTGTAACTTTCTCAGATTCTTAAAT 513
QY 403 TATTATGAAAAAGTTTGTCTGATCACTTACATCAATATCAAGATGCA 462
DB 512 TATTATGAAAAAGTTTGTCTGATCACTTACATCAATATCAAGATGCA 453

QY 463 CACTGAATATCAAAAGAAATTAATCTAATTAAGACACAAACCTGATATT 522
DB 452 CACTGAATATCAAAAGAAATTAATCTAATTAAGACACAAACCTGATATT 393

QY 523 GTCCATCTGCTCTTTAAGCAATGTATTTCTTGCAACCCCTACACAAAGCCAG 582
DB 392 GTCCATCTGCTCTTTAAGCAATGTATTTCTTGCAACCCCTACACAAAGCCAG 333

QY 583 AAATTACACAAGTACTAGTTTATGTTATTCACGAGAGTGAATCTGAAGAGAAG 642
DB 332 AAATTACACAAGTACTAGTTTATGTTATTCACGAGAGTGAATCTGAAGAGAAG 273

QY 643 CTGTCTTTTACTACACCAATTTTACTCTTTCTTGCAATTAATCTTCTGTAGAT 702
DB 272 CTGTCTTTTACTACACCAATTTTACTCTTTCTTGCAATTAATCTTCTGTAGAT 213

QY 703 AAGTCTGTAGAAAACAGCTGTGTATTTATAGAAAACAAATTTATCTTCATCACAAGG 762
DB 212 AAGTCTGTAGAAAACAGCTGTGTATTTATAGAAAACAAATTTATCTTCATCACAAGG 153

QY 763 AAATTCATTACTTAATGCCAAATTAATACGTTTGATG 800
DB 152 AAATTCATTACTTAATGCCAAATTAATACGTTTGATG 115

RESULT 15

US-09-909-650A-23/c
; Sequence 23, Application US/09909650A
; Patent No. US20020165386A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Inc.
; APPLICANT: Fournier, Alain
; APPLICANT: Maury, Isabelle
; APPLICANT: Zhou-Liu, Qing
; APPLICANT: Desaulis-Cremont, Francine
; TITLE OF INVENTION: New Polypeptides Derived From JNK3
; FILE REFERENCE: ST99003-US-CNT-1
; CURRENT APPLICATION NUMBER: US/09/909,650A
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/FR00/00104
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/122,175
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: US 99/00586
; PRIOR FILING DATE: 1999-01-20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 1422
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-909-650A-23

Query Match 10.3%; Score 82.8; DB 3; Length 1422;

Best Local Similarity 97.7%; Pred. No. 5.5e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGCTTTTACTACACCAATTTTATGCTTTTCTTGAAATC 685
DB 1283 GCACCTGAAGAGAGGCTGCTTTTACTACACCAATTTTATGCTTTTCTTGAAATC 1224

QY 686 ATTACTTCTCTGTAGATAAGTTCTGT 711
DB 1223 ATTACTTCTCTGTAGATAAGTTCTTT 1198

QY 1223 ATTACTTCTCTGTAGATAAGTTCTTT 1198

RESULT 16

US-09-165-522-1/c
; Sequence 1, Application US/09165522
; Publication No. US2003002390A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Roger J.
; Flavel, Richard A.

Rakic, Pasco
Whitmarsh, Alan
Kuan, Chia-Yi
Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Faese, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1505 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 68...1459
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-165-522-1
Query Match 10.3%; Score 82.8; DB 3; Length 1505;
Best Local Similarity 97.7%; Pred. No. 5.6e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GTACCTGAAGAGGAGGCTGCTCTTTTACACACATTTTATGCTTTCTTCTGAATTC 685
DB 1323 GCACCTGAAGAGGAGGCTGCTCTTTTACACACATTTTATGCTTTCTTCTGAATTC 1264
QY 686 ATTACTCTCTGTAGATAGTTCTGT 711
DB 1263 ATTACTCTCTGTAGATAGTTCTTT 1238
RESULT 17
US-10-641-952/c
Sequence 952, Application US/10641643
Publication No. US20040077003A1
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
Jeffrey J. Seilhamer
Susan G. Stuart
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
GENE EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO

STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 952:
SEQUENCE CHARACTERISTICS:
LENGTH: 1505 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: G1463124
SEQUENCE DESCRIPTION: SEQ ID NO: 952 :
US-10-641-643-952
Query Match 10.3%; Score 82.8; DB 8; Length 1505;
Best Local Similarity 97.7%; Pred. No. 5.6e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GTACCTGAAGAGGAGGCTGCTCTTTTACACACATTTTATGCTTTCTTCTGAATTC 685
DB 1323 GCACCTGAAGAGGAGGCTGCTCTTTTACACACATTTTATGCTTTCTTCTGAATTC 1264
QY 686 ATTACTCTCTGTAGATAGTTCTGT 711
DB 1263 ATTACTCTCTGTAGATAGTTCTTT 1238
RESULT 18
US-10-343-710-56/c
Sequence 56, Application US/10343710
Publication No. US20040087478A1
GENERAL INFORMATION:
APPLICANT: GILLEN, Clemens
APPLICANT: WETZELS, Ingrid
APPLICANT: WENNDT, Stephan
APPLICANT: WEIHE, E.
APPLICANT: SCHAEFER, M., K.-H.
TITLE OF INVENTION: SCREENING METHOD
FILE REFERENCE: 029310.52022US
CURRENT APPLICATION NUMBER: US/10/343,710
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/EP01/09011
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 157
SOFTWARE: PatentIn version 3.2
SEQ ID NO 56
LENGTH: 1505
TYPE: DNA
ORGANISM: Homo sapiens
US-10-343-710-56
Query Match 10.3%; Score 82.8; DB 8; Length 1505;
Best Local Similarity 97.7%; Pred. No. 5.6e-09;

Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGTCTTTACTACACCATTTTACTTTCTTCTGAATTC 685
DB 1323 GCACCTGAAGAGAGGCTGTCTTTACTACACCATTTTACTTTCTTCTGAATTC 1264

QY 686 ATTACTCTCTGTAGATAAGTCTGT 711
DB 1263 ATTACTCTCTGTAGATAAGTCTTT 1238

RESULT 19
US-11-180-044-1/c
Sequence 1, Application US/11180044
Publication No. US20060035303A1
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Flavell, Richard A.
APPLICANT: Rakic, Pasko
APPLICANT: Whitmarsh, Alan
APPLICANT: Kuan, Chia-Yi
APPLICANT: Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/180,044
FILING DATE: 12-JULY-2005
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1505 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 68...1459
US-11-180-044-1

Query Match 10.3%; Score 82.8; DB 16; Length 1505;
Best Local Similarity 97.7%; Pred. No. 5 6e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGTCTTTACTACACCATTTTACTTTCTTCTGAATTC 685
DB 1323 GCACCTGAAGAGAGGCTGTCTTTACTACACCATTTTACTTTCTTCTGAATTC 1264

QY 686 ATTACTCTCTGTAGATAAGTCTGT 711
DB 1263 ATTACTCTCTGTAGATAAGTCTTT 1238

RESULT 20
US-11-127-817-10/c
Sequence 10, Application US/11127817
Publication No. US20050287519A1
GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koertraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions And Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-D USA
CURRENT APPLICATION NUMBER: US/11/127,817
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 534
SOFTWARE: Patencin version 3.3
SEQ ID NO: 10
LENGTH: 2211
TYPE: DNA
ORGANISM: Homo sapiens
US-11-127-817-10

Query Match 10.3%; Score 82.8; DB 15; Length 2211;
Best Local Similarity 97.7%; Pred. No. 6 7e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGTCTTTACTACACCATTTTACTTTCTTCTGAATTC 685
DB 1323 GCACCTGAAGAGAGGCTGTCTTTACTACACCATTTTACTTTCTTCTGAATTC 1264

QY 686 ATTACTCTCTGTAGATAAGTCTGT 711
DB 1263 ATTACTCTCTGTAGATAAGTCTTT 1238

RESULT 21
US-09-165-522-3/c
Sequence 3, Application US/09165522
Publication No. US20030023990A1
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Flavell, Richard A.
APPLICANT: Rakic, Pasko
APPLICANT: Whitmarsh, Alan
APPLICANT: Kuan, Chia-Yi
APPLICANT: Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2367 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-165-522-3

Query Match 10.3%; Score 82.8; DB 3; Length 2367;
Best Local Similarity 97.7%; Pred. No. 6.9e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGTCCTTTACTACACCATTTTAGCTTTCTTCTGAATTC 685
DB 1479 GCACCTGAAGAGAGGCTGTCCTTTACTACACCATTTTAGCTTTCTTCTGAATTC 1420

QY 686 ATTACTTCTTGTAGATAGTTCTGT 711
DB 1419 ATTACTTCTTGTAGATAGTTCTTT 1394

RESULT 22
US-11-180-044-3/C
Sequence 3, Application US/11180044
Publication No. US20060035303A1
GENERAL INFORMATION:
APPLICANT: DAVIS, Roger J.
APPLICANT: Flavell, Richard A.
APPLICANT: Rakic, Pasako
APPLICANT: Whitmarsh, Alan
APPLICANT: Kuan, Chia-Yi
APPLICANT: Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/180,044
FILING DATE: 12-JULY-2005
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-OCT-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2367 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-11-180-044-3

Query Match 10.3%; Score 82.8; DB 16; Length 2367;
Best Local Similarity 97.7%; Pred. No. 6.9e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGTCCTTTACTACACCATTTTAGCTTTCTTCTGAATTC 685
DB 1479 GCACCTGAAGAGAGGCTGTCCTTTACTACACCATTTTAGCTTTCTTCTGAATTC 1420

QY 686 ATTACTTCTTGTAGATAGTTCTGT 711
DB 1419 ATTACTTCTTGTAGATAGTTCTTT 1394

RESULT 23
US-10-765-700-34/C
Sequence 34, Application US/10765700
Publication No. US20050130171A1
GENERAL INFORMATION:
APPLICANT: Loring, Jeanne F.
APPLICANT: Tingley, Debora W.
APPLICANT: Edwards, Carla M.
TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
FILE REFERENCE: PA-0024 US
CURRENT APPLICATION NUMBER: US/10/765,700
CURRENT FILING DATE: 2004-01-26
PRIOR APPLICATION NUMBER: US/09/566,921
PRIOR FILING DATE: PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL Program
SEQ ID NO 34
LENGTH: 2677
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: 413797.5
FEATURE:
NAME/KEY: unsure
LOCATION: 2024
OTHER INFORMATION: a, t, c, g, or other
US-10-765-700-34

Query Match 10.3%; Score 82.8; DB 10; Length 2677;
Best Local Similarity 97.7%; Pred. No. 7.3e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGTCCTTTACTACACCATTTTAGCTTTCTTCTGAATTC 685
DB 1795 GCACCTGAAGAGAGGCTGTCCTTTACTACACCATTTTAGCTTTCTTCTGAATTC 1736

QY 686 ATTACTTCTTGTAGATAGTTCTGT 711
DB 1735 ATTACTTCTTGTAGATAGTTCTTT 1710

RESULT 24
US-11-127-817-11/C
Sequence 11, Application US/11127817
Publication No. US20050287519A1
GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel

	Query Match	10.1%;	Score 80.4;	DB 10;	Length 972;	
	Best Local Similarity	98.8%;	Pred. No. 1.7e-08;			
Matches	81;	Conservative	0;	Mismatches	1;	Indels 0; Gaps 0
QY	628	ACGTAAGAGAAGGGGTGCCTTTTACTAACAACATTTTAACTTCCTTCTCCTCAATCAT	687			
Dd	453	AGCTGAAGAGAAGCGTGCTGCTTTTACTACACCATTTTAACTTTCTTGTAATTCAT	394			
QY	688	TACTTCCTTGTGATATAATTCT	709			
Dd	393	TACTTCCTTGTGATATAATTCT	372			

```

RESULT 27
US-10-450-763-11488/c
; Sequence 11488, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450.763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ. ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 11488
; LENGTH: 1111
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (25)..(1452)
; OTHER INFORMATION: 81% homologous to Homo sapiens putative p150, accession number
; US-10-450-763-11488

```

Query Match	10.18; Score 80.4; DB 10; Length 1111;
-------------	--

Best Local Similarity 98.8%; Pred. No. 1.8e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 628 ACCTGAGGAGAGAGGCTGCTCTTTACTACACCATTTTGTAGTCTTTCTTCTGAAATTCAT 687
DB 453 AGCTGAGGAGAGAGGCTGCTCTTTACTACACCATTTTGTAGTCTTTCTTCTGAAATTCAT 394

QY 688 TACTTCTTGTAGTAAGTTCT 709
DB 393 TACTTCTTGTAGTAAGTTCT 372

RESULT 28

US-09-909-650A-22/c
Sequence 22, Application US/09909650A
Patent No. US20020165386A1
GENERAL INFORMATION:
APPLICANT: Aventis Pharmaceuticals Inc.
APPLICANT: Fournier Alain
APPLICANT: Maury, Isabelle
APPLICANT: Zhou-Liu, Qing
TITLE OF INVENTION: Desanlis-Cremont, Francine
FILE REFERENCE: ST99003-US-CNT-1
CURRENT APPLICATION NUMBER: US/09/909,650A
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/FR00/00104
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/122,175
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: US 99/00586
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 1306
TYPE: DNA
ORGANISM: homo sapiens
US-09-909-650A-22

Query Match 10.1%; Score 80.4; DB 3; Length 1306;
Best Local Similarity 98.8%; Pred. No. 2e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAGGAGAGAGGCTGCTCTTTACTACACCATTTTGTAGTCTTTCTTCTGAAATTCATTA 689
DB 1279 CTGAGGAGAGAGGCTGCTCTTTACTACACCATTTTGTAGTCTTTCTTCTGAAATTCATTA 1220
QY 690 CTTCCTTGTAGTAAGTTCTGT 711
DB 1219 CTTCCTTGTAGTAAGTTCTTT 1198

RESULT 29

US-09-165-522-4/c
Sequence 4, Application US/09165522
Publication No. US20030023990A1
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Flavell, Richard A.
APPLICANT: Rakic, Paako
APPLICANT: Whitmarsh, Alan
APPLICANT: Kuan, Chia-Yi
APPLICANT: Yang, Di

TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1773 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 92...1357
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-165-522-4

Query Match 10.1%; Score 80.4; DB 3; Length 1773;
Best Local Similarity 98.8%; Pred. No. 2.2e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAGGAGAGAGGCTGCTCTTTACTACACCATTTTGTAGTCTTTCTTCTGAAATTCATTA 689
DB 1343 CTGAGGAGAGAGGCTGCTCTTTACTACACCATTTTGTAGTCTTTCTTCTGAAATTCATTA 1284
QY 690 CTTCCTTGTAGTAAGTTCTGT 711
DB 1283 CTTCCTTGTAGTAAGTTCTTT 1262

RESULT 30

US-10-343-710-54/c
Sequence 54, Application US/10343710
Publication No. US20040087478A1
GENERAL INFORMATION:
APPLICANT: GILLEN, Clemens
APPLICANT: WETZELS, Ingrid
APPLICANT: WENNDT, Stephan
APPLICANT: WEIHE, E.
APPLICANT: SCHAEFER, M., K.-H.
TITLE OF INVENTION: SCREENING METHOD
FILE REFERENCE: 029310.52022US
CURRENT APPLICATION NUMBER: US/10/343,710
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/EP01/09011
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 157
SOFTWARE: PatentIn version 3.2
SEQ ID NO 54
LENGTH: 1773
TYPE: DNA
ORGANISM: Homo sapiens
US-10-343-710-54

Query Match 10.1%; Score 80.4; DB 8; Length 1773;
Best Local Similarity 98.8%; Pred. No. 2.2e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTTCTTACTACACCATTTTACTTCTTCTGAAATTCATTA 689
DB 1343 CTGAAGAGAGAGGCTGCTTCTTACTACACCATTTTACTTCTTCTGAAATTCATTA 1284
QY 690 CTTCCTTGATGATTAAGTTCTGT 711
DB 1283 CTTCCTTGATGATTAAGTTCTTT 1262

RESULT 31
US-11-180-044-4/c
Sequence 4, Application US/11180044
Publication No. US20060035303A1
GENERAL INFORMATION:
APPLICANT: DAVIS, Roger J.
APPLICANT: Flavell, Richard A.
APPLICANT: Rakic, Pasiko
APPLICANT: Whitmarsh, Alan
APPLICANT: Kuan, Chia-Yi
APPLICANT: Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/180,044
FILING DATE: 12-JULY-2005
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Faese, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1773 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 92...1357
US-11-180-044-4
Query Match 10.1%; Score 80.4; DB 16; Length 1773;
Best Local Similarity 98.8%; Pred. No. 2.2e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 630 CTGAAGAGAGAGGCTGCTTCTTACTACACCATTTTACTTCTTCTGAAATTCATTA 689
DB 1343 CTGAAGAGAGAGGCTGCTTCTTACTACACCATTTTACTTCTTCTGAAATTCATTA 1284
QY 690 CTTCCTTGATGATTAAGTTCTGT 711

DB 1283 CTTCCTTGATGATTAAGTTCTTT 1262
RESULT 32
US-10-450-763-19249/c
Sequence 19249, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: HySeq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 19249
LENGTH: 1872
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIMILAR
LOCATION: (1563)..(1688)
OTHER INFORMATION: 80% homologous to Homo sapiens Human secreted protein, SEQ ID
US-10-450-763-19249
Query Match 10.1%; Score 80.4; DB 10; Length 1872;
Best Local Similarity 98.8%; Pred. No. 2.3e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 628 ACCTGAAGAGAGAGGCTGCTTCTTACTACACCATTTTACTTCTTCTGAAATTCAT 687
DB 453 ACCTGAAGAGAGAGGCTGCTTCTTACTACACCATTTTACTTCTTCTGAAATTCAT 394
QY 688 TACTTCCTTGATGATTAAGTTCT 709
DB 393 TACTTCCTTGATGATTAAGTTCT 372
RESULT 33
US-09-771-161A-87/c
Sequence 87, Application US/09771161A
Patent No. US20020110811A1
GENERAL INFORMATION:
APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PatentIn version 3.0
SEQ ID NO 87
LENGTH: 2131
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: (1)..(2131)
LOCATION: (1)..(2131)
OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'
US-09-771-161A-87


```

NAME: Faese, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 224...1489
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-165-522-7

Query Match
Best Local Similarity 10.1%; Score 80.4; DB 3; Length 2372;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTGCTTTCTTCTGAATTCATTA 689
Db 1475 CTGAAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTGCTTTCTTCTGAATTCATTA 1416
Qy 690 CTTCCTTGATAGTAAGTTCTGT 711
Db 1415 CTTCCTTGATAGTAAGTTCTTT 1394

RESULT 37
US-10-305-720-1389/c
Sequence 1389, Application US/10305720
Publication No. US20040010136A1
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressio
FILE REFERENCE: PA-0002-1 CON
CURRENT FILING DATE: 2002-11-26
PRIOR FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: 09/016,434
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL Program
SEQ ID NO 1389
LENGTH: 2372
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: GenBank ID No. US20040010136A1 9468150
US-10-305-720-1389

Query Match
Best Local Similarity 10.1%; Score 80.4; DB 7; Length 2372;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTGCTTTCTTCTGAATTCATTA 689
Db 1475 CTGAAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTGCTTTCTTCTGAATTCATTA 1416
Qy 690 CTTCCTTGATAGTAAGTTCTGT 711
Db 1415 CTTCCTTGATAGTAAGTTCTTT 1394

RESULT 38
US-10-466-162-5/c
Sequence 5, Application US/10466162
Publication No. US20050170343A1
```

```

GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: Modulating Insulin Receptor Signaling
FILE REFERENCE: EX02-001C-PC
CURRENT FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: US 60/261,335
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,694
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,532
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,361
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,531
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,457
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,226
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,304
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,459
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,456
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 2372
TYPE: DNA
ORGANISM: Homo sapiens
US-10-466-162-5

Query Match
Best Local Similarity 10.1%; Score 80.4; DB 10; Length 2372;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTGCTTTCTTCTGAATTCATTA 689
Db 1475 CTGAAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTGCTTTCTTCTGAATTCATTA 1416
Qy 690 CTTCCTTGATAGTAAGTTCTGT 711
Db 1415 CTTCCTTGATAGTAAGTTCTTT 1394

RESULT 39
US-10-723-681-9/c
Sequence 9, Application US/10723681
Publication No. US20050192239A1
GENERAL INFORMATION:
APPLICANT: ROTH, RICHARD B.
APPLICANT: NELSON, MATTHEW ROBERTS
APPLICANT: BRAUN, ANDREAS
APPLICANT: KAMMERER, STERAN M.
APPLICANT: RENELAND, RIKARD
TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND
FILE REFERENCE: SEO-4069-CP
CURRENT FILING DATE: 2003-11-25
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: US 60/429,136
PRIOR FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: US 60/490,234
PRIOR FILING DATE: 2003-07-24
NUMBER OF SEQ ID NOS: 835
SOFTWARE: PatentIn version 3.2
SEQ ID NO 9
LENGTH: 2372
TYPE: DNA
ORGANISM: Homo sapiens
```

US-10-723-681-9

Query Match 10.1%; Score 80.4; DB 10; Length 2372;
Best Local Similarity 98.8%; Pred. No. 2.6e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTCATTA 689
DB 1475 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTCATTA 1416
QY 690 CTTCCTGTAGATAGTCTGT 711
DB 1415 CTTCCTGTAGATAGTCTTT 1394

RESULT 40

US-10-857-780-11/c
Sequence 11, Application US/10857780
Publication No. US20050272043A1

GENERAL INFORMATION:
APPLICANT: ROTH, RICHARD B.
APPLICANT: BRAUN, ANDREAS
APPLICANT: KAMMERER, STEFAN M.
APPLICANT: NELSON, MATTHEW ROBERTS
APPLICANT: RENELAND, RICHARD HENRY
APPLICANT: HOVAL-WRIGHTSON, CAROLYN R.
TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
FILE REFERENCE: SEQ-4069-CP
CURRENT APPLICATION NUMBER: US/10/857,780
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: 10/723,681
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR FILING DATE: 2003-07-24
PRIOR APPLICATION NUMBER: 60/525,239
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 4962
SOFTWARE: PatentIn version 3.2
SEQ ID NO 11
LENGTH: 2372
TYPE: DNA
ORGANISM: Homo sapiens

US-10-857-780-11

Query Match 10.1%; Score 80.4; DB 10; Length 2372;
Best Local Similarity 98.8%; Pred. No. 2.6e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTCATTA 689
DB 1475 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTCATTA 1416
QY 690 CTTCCTGTAGATAGTCTGT 711
DB 1415 CTTCCTGTAGATAGTCTTT 1394

RESULT 41

US-11-127-817-9/c

Sequence 9, Application US/11127817
Publication No. US20050287519A1

GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koentraad F. F.
APPLICANT: laenen, Wendy
TITLE OF INVENTION: Methods, Compositions And Compound Assays For Inhibiting
FILE REFERENCE: P27,800-D USA
CURRENT APPLICATION NUMBER: US/11/127,817
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352

PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 534
SOFTWARE: PatentIn version 3.3
SEQ ID NO 9
LENGTH: 2372
TYPE: DNA
ORGANISM: Homo sapiens

US-11-127-817-9

Query Match 10.1%; Score 80.4; DB 15; Length 2372;
Best Local Similarity 98.8%; Pred. No. 2.6e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTCATTA 689
DB 1475 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTCATTA 1416
QY 690 CTTCCTGTAGATAGTCTGT 711
DB 1415 CTTCCTGTAGATAGTCTTT 1394

RESULT 42

US-11-180-044-6/c
Sequence 6, Application US/11180044
Publication No. US20060035303A1

GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Flavell, Richard A.
APPLICANT: Rakic, Pasko
APPLICANT: Whitmarsh, Alan
APPLICANT: Kuan, Chia-Yi
APPLICANT: Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P. C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/180,044
FILING DATE: 12-JULY-2005
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA

US-11-180-044-6

Query Match 10.1%; Score 80.4; DB 16; Length 2372;
Best Local Similarity 98.8%; Pred. No. 2.6e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTCTTACTACACATTTTACTGTTCTTCTGAAATTCATTA 689
DB 1475 CTGAAGAGAGAGGCTGCTCTTCTTACTACACATTTTACTGTTCTTCTGAAATTCATTA 1416

QY 690 CTTCTTGTAGATAAGTTCTGT 711
DB 1415 CTTCTTGTAGATAAGTTCTTT 1394

RESULT 43

US-11-180-044-7/c
Sequence 7, Application US/11180044
Publication No. US20060035303A1

GENERAL INFORMATION:

APPLICANT: Davis, Roger J.

APPLICANT: Flavell, Richard A.

APPLICANT: Rakic, Pasiko

APPLICANT: Whitmarsh, Alan

APPLICANT: Kuan, Chi-Yi

APPLICANT: Yang, Di

TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: IBM Compatible

SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/180,044

FILING DATE: 12-JULY-2005

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/09/165,522

FILING DATE: 02-Oct-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/060,995

FILING DATE: 03-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Pasase, J. Peter

REGISTRATION NUMBER: 32,983

REFERENCE/DOCKET NUMBER: 10363/005001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 2372 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 224...1489

US-11-180-044-7

Query Match 10.1%; Score 80.4; DB 16; Length 2372;
Best Local Similarity 98.8%; Pred. No. 2.6e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTCTTACTACACATTTTACTGTTCTTCTGAAATTCATTA 689
DB 1475 CTGAAGAGAGAGGCTGCTCTTCTTACTACACATTTTACTGTTCTTCTGAAATTCATTA 1416

QY 690 CTTCTTGTAGATAAGTTCTGT 711
DB 1415 CTTCTTGTAGATAAGTTCTTT 1394

RESULT 44

US-10-765-700-33/c

Sequence 33, Application US/10765700

Publication No. US20050130171A1

GENERAL INFORMATION:

APPLICANT: Loring, Jeanne F.

APPLICANT: Tingley, Debora W.

APPLICANT: Edwards, Carla M.

TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE

FILE REFERENCE: PA-0024 US

CURRENT APPLICATION NUMBER: US/10/765,700

CURRENT FILING DATE: 2004-01-26

PRIOR APPLICATION NUMBER: US/09/566,921

PRIOR FILING DATE: PRIOR FILING DATE: 2000-05-05

NUMBER OF SEQ ID NOS: 138

SOFTWARE: PERL Program

SEQ ID NO 33

LENGTH: 2982

TYPE: DNA

ORGANISM: Homo sapiens

NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No: 413797.7

FEATURE:

NAME/KEY: unsure

LOCATION: 1770-1816

OTHER INFORMATION: a, t, c, g, or other

US-10-765-700-33

Query Match 10.1%; Score 80.4; DB 10; Length 2982;

Best Local Similarity 98.8%; Pred. No. 2.8e-08;

Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTCTTACTACACATTTTACTGTTCTTCTGAAATTCATTA 689

DB 1570 CTGAAGAGAGAGGCTGCTCTTCTTACTACACATTTTACTGTTCTTCTGAAATTCATTA 1511

QY 690 CTTCTTGTAGATAAGTTCTGT 711

DB 1510 CTTCTTGTAGATAAGTTCTTT 1489

RESULT 45

US-09-776-167A-8/c

Sequence 8, Application US/09776167A

Patent No. US20020058243A1

GENERAL INFORMATION:

APPLICANT: Jarnigan, Kurt

APPLICANT: Greene, Amy

TITLE OF INVENTION: RAPID, PARALLEL IDENTIFICATION OF CELL LINES

FILE REFERENCE: 0024 US

CURRENT APPLICATION NUMBER: US/09/776,167A

CURRENT FILING DATE: 2001-05-21

PRIOR APPLICATION NUMBER: USSN 60/179,893

PRIOR FILING DATE: 2000-02-02

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn version 3.0

SEQ ID NO 8

LENGTH: 8750

TYPE: DNA

ORGANISM: pFastFind-JNK3

US-09-776-167A-8

Query Match 10.1%; Score 80.4; DB 3; Length 8750;

Best Local Similarity 98.8%; Pred. No. 4.6e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 630 CTGAAGAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTTCTGAATTCATTA 689
Db 1782 CTGAAGAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTTCTGAATTCATTA 1723

Qy 690 CTTCCTGTAGATAGTTCTGT 711
Db 1722 CTTCCTGTAGATAGTTCTTT 1701

RESULT 46

US-11-136-527-4334/c
Sequence 4334, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4334
LENGTH: 600
TYPE: DNA
ORGANISM: Rattus norvegicus
US-11-136-527-4334

Query Match 8.3%; Score 66.8; DB 16; Length 600;
Best Local Similarity 86.0%; Pred. No. 2.4e-05;
Matches 74; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 626 GTACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTTCTGAATTC 685
Db 125 GCACCTGAAGAGGCTGCGCTTGTGACTACCGCGTCTTCTTCTTCTGAGTTC 66

Qy 686 ATTACTCTCTGTAGATAGTTCTGT 711
Db 65 ATTACTCTCTGTAGATAGTTCTTT 40

RESULT 47

US-09-165-522-9/c
Sequence 9, Application US/09165522
Publication No. US20030023990A1
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Flavell, Richard A.
APPLICANT: Rakic, Paeko
APPLICANT: Whitmarsh, Alan
APPLICANT: Xuan, Chia-Yi

TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522

FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Passe, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 1975 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 364...1641
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-165-522-9

Query Match 8.3%; Score 66.8; DB 3; Length 1975;
Best Local Similarity 86.0%; Pred. No. 4e-05;
Matches 74; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 626 GTACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTTCTGAATTC 685
Db 1505 GCACCTGAAGAGGCTGCGCTTGTGACTACCGCGTCTTCTTCTTCTGAGTTC 1446

Qy 686 ATTACTCTCTGTAGATAGTTCTGT 711
Db 1445 ATTACTCTCTGTAGATAGTTCTTT 1420

RESULT 48

US-10-343-710-60/c
Sequence 60, Application US/10343710
Publication No. US20040087478A1
GENERAL INFORMATION:
APPLICANT: GILLEN, Clemens
APPLICANT: WETZELS, Ingrid
APPLICANT: WENDEL, Stephan
APPLICANT: WEIHE, E.
APPLICANT: SCHAEFER, M., K.-H.

TITLE OF INVENTION: SCREENING METHOD
FILE REFERENCE: 029310.52022US
CURRENT APPLICATION NUMBER: US/10/343,710
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/EP01/09011
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 157
SOFTWARE: PatentIn version 3.2
SEQ ID NO 60
LENGTH: 1975
TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-343-710-60

Query Match 8.3%; Score 66.8; DB 8; Length 1975;
Best Local Similarity 86.0%; Pred. No. 4e-05;
Matches 74; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 626 GTACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTTCTGAATTC 685
Db 1505 GCACCTGAAGAGGCTGCGCTTGTGACTACCGCGTCTTCTTCTTCTGAGTTC 1446

Qy 686 ATTACTCTCTGTAGATAGTTCTGT 711
Db 1445 ATTACTCTCTGTAGATAGTTCTTT 1420

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2006, 19:46:54 ; Search time 166 Seconds
(without alignments)
6923.085 Million cell updates/sec

Title: US10723681MOD.SEQ

Perfect score: 800
Sequence: 1 acctttcccaaacctctta.....caataatcagcttttgacg 800

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 899801 seqs, 718270062 residues

Total number of hits satisfying chosen parameters: 1799602

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications NA New.*
1: /EMC_Celerra_SIDS3/prodata/1/pubpna/US09_NEW_PUB.seq.*
2: /EMC_Celerra_SIDS3/prodata/1/pubpna/US06_NEW_PUB.seq.*
3: /EMC_Celerra_SIDS3/prodata/1/pubpna/US07_NEW_PUB.seq.*
4: /EMC_Celerra_SIDS3/prodata/1/pubpna/US08_NEW_PUB.seq.*
5: /EMC_Celerra_SIDS3/prodata/1/pubpna/US10_NEW_PUB.seq.*
6: /EMC_Celerra_SIDS3/prodata/1/pubpna/US11_NEW_PUB.seq.*
7: /EMC_Celerra_SIDS3/prodata/1/pubpna/US11_NEW_PUB.seq.*
8: /EMC_Celerra_SIDS3/prodata/1/pubpna/US11_NEW_PUB.seq.*
9: /EMC_Celerra_SIDS3/prodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	82.8	10.3	1000	US-11-266-748A-223967	Sequence 223967, A
C 2	82.8	10.3	1000	US-11-266-748A-292324	Sequence 292324, A
C 3	82.8	10.3	1000	US-11-266-748A-343753	Sequence 343753, A
C 4	82.8	10.3	1000	US-11-266-748A-403979	Sequence 403979, A
C 5	82.8	10.3	1000	US-11-266-748A-403980	Sequence 403980, A
C 6	82.8	10.3	1000	US-11-266-748A-475025	Sequence 475025, A
C 7	82.8	10.3	1000	US-11-266-748A-475026	Sequence 475026, A
C 8	82.8	10.3	2211	US-11-266-748A-571178	Sequence 571178, A
C 9	82.8	10.3	2698	US-11-266-748A-331164	Sequence 331164, A
C 10	82.8	10.3	3232	US-11-266-748A-349578	Sequence 349578, A
C 11	82.8	10.3	3232	US-11-266-748A-382414	Sequence 382414, A
C 12	82.8	10.3	3232	US-11-266-748A-432957	Sequence 432957, A
C 13	50	6.2	801	US-11-266-748A-46908	Sequence 46908, A
C 14	48.4	6.0	1000	US-11-266-748A-403999	Sequence 403999, A
C 15	48.4	6.0	1000	US-11-266-748A-475045	Sequence 475045, A
C 16	48.4	6.0	1180	US-11-266-748A-69204	Sequence 69204, A
C 17	48.4	6.0	1180	US-11-266-748A-105295	Sequence 105295, A
C 18	48.4	6.0	1180	US-11-266-748A-132015	Sequence 132015, A
C 19	48.4	6.0	1928	US-11-266-748A-349487	Sequence 349487, A
C 20	48.4	6.0	1928	US-11-266-748A-432866	Sequence 432866, A
C 21	48.4	6.0	1942	US-11-283-329-225	Sequence 225, App
C 22	48.4	6.0	1942	US-11-283-329-231	Sequence 231, App
C 23	48.4	6.0	2251	US-11-266-748A-182241	Sequence 182241, A
C 24	48.4	6.0	2251	US-11-266-748A-242782	Sequence 242782, A

C 25	46.8	5.8	1947	8	US-11-283-329-227	Sequence 227, App
C 26	46.8	5.8	1947	8	US-11-283-329-229	Sequence 229, App
C 27	44.4	5.5	1412	8	US-11-283-329-217	Sequence 217, App
C 28	44.4	5.5	1412	8	US-11-283-329-223	Sequence 223, App
C 29	43.2	5.4	1676	6	US-10-449-902-24462	Sequence 24462, A
C 30	42	5.2	1000	8	US-11-266-748A-395934	Sequence 395934, A
C 31	42	5.2	1000	8	US-11-266-748A-466980	Sequence 466980, A
C 32	42	5.2	1417	8	US-11-283-329-219	Sequence 219, App
C 33	42	5.2	1417	8	US-11-283-329-221	Sequence 221, App
C 34	42	5.2	1943	8	US-11-266-748A-349577	Sequence 349577, A
C 35	42	5.2	1943	8	US-11-266-748A-382413	Sequence 382413, A
C 36	42	5.2	1943	8	US-11-266-748A-432956	Sequence 432956, A
C 37	42	5.2	3620	8	US-11-266-748A-243382	Sequence 243382, A
C 38	41.2	5.2	807	8	US-11-216-545-1069	Sequence 1069, App
C 39	41	5.1	570	8	US-11-266-748A-207992	Sequence 207992, A
C 40	40.8	5.1	139326	6	US-10-539-228-134	Sequence 134, App
C 41	40.4	5.0	1582	8	US-11-222-810-10	Sequence 10, App
C 42	40.4	5.0	1582	8	US-11-222-810-12	Sequence 12, App
C 43	39.6	5.0	557	8	US-11-266-748A-41216	Sequence 41216, A
C 44	39.6	5.0	559	8	US-11-266-748A-95203	Sequence 95203, A
C 45	39.6	5.0	559	8	US-11-266-748A-148014	Sequence 148014, A
C 46	39.6	5.0	1000	8	US-11-266-748A-117427	Sequence 117427, A
C 47	39.6	5.0	1000	8	US-11-266-748A-159591	Sequence 159591, A
C 48	39.6	5.0	1000	8	US-11-266-748A-222651	Sequence 222651, A
C 49	39.6	5.0	1000	8	US-11-266-748A-289193	Sequence 289193, A
C 50	39.6	5.0	1000	8	US-11-266-748A-340622	Sequence 340622, A
C 51	39.6	5.0	1000	8	US-11-266-748A-400178	Sequence 400178, A
C 52	39.6	5.0	1000	8	US-11-266-748A-471224	Sequence 471224, A
C 53	39.6	5.0	3091	6	US-10-517-441-483	Sequence 483, App
C 54	39.6	5.0	3091	6	US-10-517-441-757	Sequence 757, App
C 55	39.6	5.0	3216	6	US-10-511-937-609	Sequence 609, App
C 56	39.6	5.0	6101	6	US-10-517-441-705	Sequence 705, App
C 57	39.2	4.9	11429	6	US-10-517-441-480	Sequence 480, App
C 58	39.2	4.9	11429	6	US-10-517-441-754	Sequence 754, App
C 59	38.6	4.8	1973	8	US-11-216-545-582	Sequence 582, App
C 60	38.6	4.8	8900	6	US-10-517-441-427	Sequence 427, App
C 61	38.4	4.8	8900	6	US-10-517-441-701	Sequence 701, App
C 62	38.4	4.8	604	8	US-11-266-748A-51538	Sequence 51538, A
C 63	38.4	4.8	661	8	US-11-266-748A-12709	Sequence 12709, A
C 64	38.4	4.8	1000	8	US-11-266-748A-291112	Sequence 291112, A
C 65	38.4	4.8	1000	8	US-11-266-748A-402451	Sequence 402451, A
C 66	38.4	4.8	1000	8	US-11-266-748A-402493	Sequence 402493, A
C 67	38.4	4.8	1000	8	US-11-266-748A-473539	Sequence 473539, A
C 68	38.4	4.8	1228	8	US-11-266-748A-189872	Sequence 189872, A
C 69	38.4	4.8	1228	8	US-11-266-748A-243474	Sequence 243474, A
C 70	38.4	4.8	2875	8	US-11-266-748A-30798	Sequence 30798, A
C 71	38	4.8	852	8	US-11-216-545-385	Sequence 385, App
C 72	38	4.8	6101	6	US-10-517-441-431	Sequence 431, App
C 73	37.8	4.7	481	6	US-10-486-020-36	Sequence 36, App
C 74	37.8	4.7	8093	6	US-10-517-441-308	Sequence 308, App
C 75	37.8	4.7	8093	6	US-10-517-441-582	Sequence 582, App
C 76	37.8	4.7	162351	6	US-11-266-748A-334317	Sequence 334317, A
C 77	37.6	4.7	394191	6	US-10-506-549-3	Sequence 3, App
C 78	37.6	4.7	945	6	US-10-471-571A-1599	Sequence 1599, App
C 79	37.4	4.7	1349	8	US-11-266-748A-25040	Sequence 25040, A
C 80	37.4	4.7	2090	8	US-11-266-748A-25400	Sequence 25400, A
C 81	37.4	4.7	19634	6	US-10-517-441-414	Sequence 414, App
C 82	37.2	4.7	19634	6	US-10-517-441-688	Sequence 688, App
C 83	37.2	4.7	8169	6	US-10-517-441-270	Sequence 270, App
C 84	37.2	4.7	8169	6	US-10-517-441-544	Sequence 544, App
C 85	36.8	4.6	1000	8	US-11-266-748A-116732	Sequence 116732, A
C 86	36.8	4.6	1000	8	US-11-266-748A-158896	Sequence 158896, A
C 87	36.8	4.6	1000	8	US-11-266-748A-198820	Sequence 198820, A
C 88	36.8	4.6	1000	8	US-11-266-748A-281979	Sequence 281979, A
C 89	36.8	4.6	1649	8	US-11-266-748A-308619	Sequence 308619, A
C 90	36.8	4.6	1649	8	US-11-216-545-514	Sequence 514, App
C 91	36.8	4.6	2630	6	US-11-266-748A-27342	Sequence 27342, App
C 92	36.6	4.6	879	6	US-10-471-571A-1881	Sequence 1881, App
C 93	36.6	4.6	1607	8	US-11-216-545-1884	Sequence 1884, App
C 94	36.6	4.6	2444	7	US-11-216-305-15168	Sequence 15168, A
C 95	36.4	4.6	150024	7	US-11-266-748A-60141	Sequence 60141, A
C 96	36.4	4.5	4294	7	US-11-021-837-14	Sequence 14, App
C 97	36.4	4.5	4443	8	US-11-266-748A-24099	Sequence 24099, A

C 98 36.4 4.5 13076 6 US-10-517-441-394 Sequence 394, App
C 99 36.4 4.5 13076 6 US-10-517-441-668 Sequence 668, App
C 100 36.2 4.5 2707 8 US-11-216-545-2975 Sequence 2975, Ap

ALIGNMENTS

RESULT 1

US-11-266-748A-223967/c
; Sequence 223967, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 223967
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-223967
Query Match 10.3%; Score 82.8; DB 8; Length 1000;
Best Local Similarity 97.7%; Pred. No. 1.3e-10;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GACCTGAAGAGGAGGCTGCTTTTACTACACCATTTTGTCTTTCTTCTGAATTC 685
DB 112 GCACCTGAAGAGGAGGCTGCTTTTACTACACCATTTTGTCTTTCTTCTGAATTC 53
QY 686 ATTACTCTCTGTAGATAGTTCTGT 711
DB 52 ATTACTCTCTGTAGATAGTTCTTT 27
RESULT 2
US-11-266-748A-292324/c
; Sequence 292324, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 292324
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-292324
Query Match 10.3%; Score 82.8; DB 8; Length 1000;
Best Local Similarity 97.7%; Pred. No. 1.3e-10;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GACCTGAAGAGGAGGCTGCTTTTACTACACCATTTTGTCTTTCTTCTGAATTC 685
DB 112 GCACCTGAAGAGGAGGCTGCTTTTACTACACCATTTTGTCTTTCTTCTGAATTC 53
QY 686 ATTACTCTCTGTAGATAGTTCTGT 711
DB 52 ATTACTCTCTGTAGATAGTTCTTT 27

RESULT 3

US-11-266-748A-343753
; Sequence 343753, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 343753
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-343753
Query Match 10.3%; Score 82.8; DB 8; Length 1000;

```
Best Local Similarity 97.7%; Pred. No. 1.3e-10;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTCTGAATTC 685
   |||||
Db 889 GCACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTCTGAATTC 948

QY 686 ATTACTCTCTGTAGATAGTTCTGT 711
   |||||
Db 949 ATTACTCTCTGTAGATAGTTCTTT 974

RESULT 4
US-11-266-748A-403979/c
; Sequence 403979, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 403979
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-403979

Query Match 10.3%; Score 82.8; DB 8; Length 1000;
Best Local Similarity 97.7%; Pred. No. 1.3e-10;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTCTGAATTC 685
   |||||
Db 112 GCACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTCTGAATTC 53

QY 686 ATTACTCTCTGTAGATAGTTCTGT 711
   |||||
Db 52 ATTACTCTCTGTAGATAGTTCTTT 27

RESULT 5
US-11-266-748A-403980/c
; Sequence 403980, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
```

```
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 403980
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-403980

Query Match 10.3%; Score 82.8; DB 8; Length 1000;
Best Local Similarity 97.7%; Pred. No. 1.3e-10;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTCTGAATTC 685
   |||||
Db 112 GCACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTCTGAATTC 53

QY 686 ATTACTCTCTGTAGATAGTTCTGT 711
   |||||
Db 52 ATTACTCTCTGTAGATAGTTCTTT 27

RESULT 6
US-11-266-748A-475025
; Sequence 475025, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 475025
; LENGTH: 1000
; TYPE: DNA
```

```
; ORGANISM: Homo Sapiens
US-11-266-748A-475026

Query Match
Best Local Similarity 97.7%; Pred. No. 1.3e-10;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 626 GTACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTCTGAATTC 685
Db 889 GCACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTCTGAATTC 948

Qy 686 ATTACTCTCTGTAGATAGTCTGT 711
Db 949 ATTACTCTCTGTAGATAGTCTTT 974

RESULT 7
US-11-266-748A-475026
; Sequence 475026, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 475026
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-475026

Query Match
Best Local Similarity 97.7%; Pred. No. 1.3e-10;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 626 GTACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTCTGAATTC 685
Db 889 GCACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTCTGAATTC 948

Qy 686 ATTACTCTCTGTAGATAGTCTGT 711
Db 949 ATTACTCTCTGTAGATAGTCTTT 974

RESULT 8
US-11-266-748A-57178/C
; Sequence 57178, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
```

```
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 57178
; LENGTH: 2211
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-57178

Query Match
Best Local Similarity 97.7%; Pred. No. 1.6e-10;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 626 GTACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTCTGAATTC 685
Db 1323 GCACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTCTGAATTC 1264

Qy 686 ATTACTCTCTGTAGATAGTCTGT 711
Db 1263 ATTACTCTCTGTAGATAGTCTTT 1238

RESULT 9
US-11-266-748A-31164/C
; Sequence 31164, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
```

```
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 31164
/ LENGTH: 2698
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
US-11-266-748A-31164

Query Match      10.3%; Score 82.8; DB 8; Length 2698;
Best Local Similarity 97.7%; Pred. No. 1.7e-10;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTAACTCTTTCTTGAATTC 685
DB 1810 GCACCTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTAACTCTTTCTTGAATTC 1751

QY 686 ATTACTCTCTGTAGATAGTTCGT 711
DB 1750 ATTACTCTCTGTAGATAGTTCGT 1725

RESULT 10
US-11-266-748A-349578/c
/ Sequence 349578, Application US/11266748A
/ Publication No. US20060134663A1
/ GENERAL INFORMATION:
/ APPLICANT: Harkin, Paul
/ APPLICANT: Johnson, Patrick
/ APPLICANT: Mulligan, Karl
/ TITLE OF INVENTION: Transcriptional Microarray Technology and
/ FILE REFERENCE: 55815-0102 (319189)
/ CURRENT APPLICATION NUMBER: US/11/266,748A
/ PRIOR FILING DATE: 2005-11-03
/ PRIOR APPLICATION NUMBER: EP 04105479.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105482.6
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105483.4
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105507.0
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105485.9
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105484.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: US 60/662,276
/ PRIOR FILING DATE: 2005-03-14
/ PRIOR APPLICATION NUMBER: US 60/700,293
/ PRIOR FILING DATE: 2005-07-18
/ NUMBER OF SEQ ID NOS: 483996
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 349578
/ LENGTH: 3232
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (161)..(201)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1979)..(2028)
/ OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-349578

Query Match      10.3%; Score 82.8; DB 8; Length 3232;
Best Local Similarity 97.7%; Pred. No. 1.8e-10;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTAACTCTTTCTTGAATTC 685
DB 1788 GCACCTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTAACTCTTTCTTGAATTC 1729
```

```
QY 686 ATTACTCTCTGTAGATAGTTCGT 711
DB 1728 ATTACTCTCTGTAGATAGTTCGT 1703

RESULT 11
US-11-266-748A-382414/c
/ Sequence 382414, Application US/11266748A
/ Publication No. US20060134663A1
/ GENERAL INFORMATION:
/ APPLICANT: Harkin, Paul
/ APPLICANT: Johnson, Patrick
/ APPLICANT: Mulligan, Karl
/ TITLE OF INVENTION: Transcriptional Microarray Technology and
/ FILE REFERENCE: 55815-0102 (319189)
/ CURRENT APPLICATION NUMBER: US/11/266,748A
/ PRIOR FILING DATE: 2005-11-03
/ PRIOR APPLICATION NUMBER: EP 04105479.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105482.6
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105483.4
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105507.0
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105485.9
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105484.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: US 60/662,276
/ PRIOR FILING DATE: 2005-03-14
/ PRIOR APPLICATION NUMBER: US 60/700,293
/ PRIOR FILING DATE: 2005-07-18
/ NUMBER OF SEQ ID NOS: 483996
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 382414
/ LENGTH: 3232
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (161)..(201)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1979)..(2028)
/ OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-382414

Query Match      10.3%; Score 82.8; DB 8; Length 3232;
Best Local Similarity 97.7%; Pred. No. 1.8e-10;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTAACTCTTTCTTGAATTC 685
DB 1788 GCACCTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTAACTCTTTCTTGAATTC 1729

QY 686 ATTACTCTCTGTAGATAGTTCGT 711
DB 1728 ATTACTCTCTGTAGATAGTTCGT 1703

RESULT 12
US-11-266-748A-432957
/ Sequence 432957, Application US/11266748A
/ Publication No. US20060134663A1
/ GENERAL INFORMATION:
/ APPLICANT: Harkin, Paul
/ APPLICANT: Johnson, Patrick
/ APPLICANT: Mulligan, Karl
/ TITLE OF INVENTION: Transcriptional Microarray Technology and
```

```
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
PRIOR FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 432957
LENGTH: 3232
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1205)..(1254)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc.feature
LOCATION: (3032)..(3072)
OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-432957

Query Match
Best Local Similarity 10.3%; Score 82.8; DB 8; Length 3232;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 626 GTACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTGAATTC 685
Db 1445 GCACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTGAATTC 1504
Qy 686 ATTACTCTGTAGATAGTCTGT 711
Db 1505 ATTACTCTGTAGATAGTCTGT 1530

RESULT 13
US-11-266-748A-46908/c
Sequence 46908, Application US/11266748A
Publication No. US2006013463A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
TITLE OF INVENTION: Transcription Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
```

```

PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 46908
LENGTH: 801
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-46908
```

```
Query Match
Best Local Similarity 6.2%; Score 50; DB 8; Length 801;
Matches 62; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
```

```
Qy 630 CTGAAGAGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTGAATTCATTA 689
Db 431 CTGCATCTGAAGGCTGATCTTTTACTACACCATTTCTTCTTCCCAATCATGA 372
Qy 690 CTTCCTGTAGATAGTCTGT 711
Db 371 CTTCCTGTAGATAGTCTGT 350
```

```
RESULT 14
US-11-266-748A-403999/c
Sequence 403999, Application US/11266748A
Publication No. US2006013463A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
TITLE OF INVENTION: Transcription Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 403999
LENGTH: 1000
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-403999

Query Match
Best Local Similarity 6.0%; Score 48.4; DB 8; Length 1000;
Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
```

```
RESULT 15
US-11-266-748A-475045
; Sequence 475045, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 475045
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-475045

Query Match      6.0%; Score 48.4; DB 8; Length 1000;
Best Local Similarity 74.4%; Pred. No. 0.028;
Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy      630 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTGCTTTCTTCTGCAATTCATTA 689
      756 CTGCATCTGAAGGCTGATCTTTTACACACCATTTCTGCTTTCTTCCCAATCCATCA 815
      816 CTTCTTTGTAATTAAGCTCTTT 837

Db

RESULT 16
US-11-266-748A-69204/c
; Sequence 69204, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
```

```

; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 69204
; LENGTH: 1180
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-69204

Query Match      6.0%; Score 48.4; DB 8; Length 1180;
Best Local Similarity 74.4%; Pred. No. 0.03;
Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy      630 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTGCTTTCTTCTGCAATTCATTA 689
      431 CTGCATCTGAAGGCTGATCTTTTACACACCATTTCTGCTTTCTTCCCAATCCATCA 372
      371 CTTCTTTGTAATTAAGCTCTTT 350

Db

RESULT 17
US-11-266-748A-105295/c
; Sequence 105295, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 105295
; LENGTH: 1180
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-105295

Query Match      6.0%; Score 48.4; DB 8; Length 1180;
Best Local Similarity 74.4%; Pred. No. 0.03;
Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy      630 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTGCTTTCTTCTGCAATTCATTA 689
      431 CTGCATCTGAAGGCTGATCTTTTACACACCATTTCTGCTTTCTTCCCAATCCATCA 372
      372 CTTCTTTGTAATTAAGCTCTTT 350

Db
```


FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266, 748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 48396
SOFTWARE: PatentIn version 3.3
SEQ ID NO 242782
LENGTH: 2251
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-242782

Query Match 6.0%; Score 48.4; DB 8; Length 2251;
Best Local Similarity 74.4%; Pred. No. 0.036;
Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTCTGGAATTCATTA 689
DB 1954 CTGCACTGAGAGGCTGATCTTTTACAAACACCATTTGCTTCTTCCCAATTCATGA 2013
QY 690 CTTCCTGTAGATAGTCTGT 711
DB 2014 CTTCCTGTAAATTAAGCTCTT 2035

RESULT 25
US-11-283-329-227/c
Sequence 227, Application US/11283329
Publication No. US20060134670A1
GENERAL INFORMATION:
APPLICANT: Piu, Fabrice
TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
FILE REFERENCE: ACADIA.043A
CURRENT APPLICATION NUMBER: US/11/283,329
CURRENT FILING DATE: 2005-11-18
PRIOR APPLICATION NUMBER: 60/629,811
PRIOR FILING DATE: 2004-11-19
NUMBER OF SEQ ID NOS: 242
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 227
LENGTH: 1947
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (50)...(1198)
OTHER INFORMATION: JNK2 variant 2
US-11-283-329-227

Query Match 5.8%; Score 46.8; DB 8; Length 1947;
Best Local Similarity 77.0%; Pred. No. 0.085;
Matches 57; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 638 GAAGGCTGTCTTTACTACACCATTTTGTCTTCTGGAATTCATTCCTTG 697
DB 1179 GAAGGCTGATCTTTTACAAACACCATTTGCTTCTTCCCAATTCATGACTCTTG 1120

QY 698 TAGATAGTCTGT 711
DB 1119 TAAATTAAGCTCTT 1106

RESULT 26
US-11-283-329-229/c
Sequence 229, Application US/11283329
Publication No. US20060134670A1
GENERAL INFORMATION:
APPLICANT: Piu, Fabrice
TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
FILE REFERENCE: ACADIA.043A
CURRENT APPLICATION NUMBER: US/11/283,329
CURRENT FILING DATE: 2005-11-18
PRIOR APPLICATION NUMBER: 60/629,811
PRIOR FILING DATE: 2004-11-19
NUMBER OF SEQ ID NOS: 242
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 229
LENGTH: 1947
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (50)...(1198)
OTHER INFORMATION: JNK2 variant 3
US-11-283-329-229

Query Match 5.8%; Score 46.8; DB 8; Length 1947;
Best Local Similarity 77.0%; Pred. No. 0.085;
Matches 57; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 638 GAAGGCTGTCTTTACTACACCATTTTGTCTTCTGGAATTCATTCCTTG 697
DB 1179 GAAGGCTGATCTTTTACAAACACCATTTGCTTCTTCCCAATTCATGACTCTTG 1120
QY 698 TAGATAGTCTGT 711
DB 1119 TAAATTAAGCTCTT 1106

RESULT 27
US-11-283-329-217/c
Sequence 217, Application US/11283329
Publication No. US20060134670A1
GENERAL INFORMATION:
APPLICANT: Piu, Fabrice
TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
FILE REFERENCE: ACADIA.043A
CURRENT APPLICATION NUMBER: US/11/283,329
CURRENT FILING DATE: 2005-11-18
PRIOR APPLICATION NUMBER: 60/629,811
PRIOR FILING DATE: 2004-11-19
NUMBER OF SEQ ID NOS: 242
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 217
LENGTH: 1412
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (18)...(1301)
OTHER INFORMATION: JNK1 variant 1
US-11-283-329-217

Query Match 5.5%; Score 44.4; DB 8; Length 1412;
Best Local Similarity 69.8%; Pred. No. 0.29;
Matches 60; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 626 GTACTGAAGAGAGGCTGTCTTTACTACACCATTTTGTCTTCTGGAATTC 685

Db 1159 GCACCTAAAGAGAGGGGCTCCCCGATTAACCTCATTCTGTTCTCTCTCCAGTCC 1100
QY 686 ATTACTTCTTGTAGTAAGTTCTGT 711
Db 1099 ATAACTTCTTATATATCAATCTTT 1074

RESULT 28

US-11-283-329-223/C
; Sequence 223, Application US/11283329
; Publication No. US20060134670A1
; GENERAL INFORMATION:
; APPLICANT: Plu, Fabrice
; TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
; FILE REFERENCE: ACADIA.043A
; CURRENT APPLICATION NUMBER: US/11/283,329
; PRIOR FILING DATE: 2005-11-18
; PRIOR APPLICATION NUMBER: 60/629,811
; PRIOR FILING DATE: 2004-11-19
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 223
; LENGTH: 1412
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)...(1301)
; OTHER INFORMATION: JNK1 variant 4
US-11-283-329-223

Query Match 5.5%; Score 44.4; DB 8; Length 1412;
Best Local Similarity 69.8%; Pred. No. 0.29;
Matches 60; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGCTCTTACTACACCACTTTTGTCTCTTCTCTGATTC 685
DB 1159 GCACCTAAAGAGAGGGCTCCCCGATTAACCTCATTCTGTTCTCTCTCCAGTCC 1100
QY 686 ATTACTTCTTGTAGTAAGTTCTGT 711
Db 1099 ATAACTTCTTATATATCAATCTTT 1074

RESULT 29

US-10-449-902-24462/C
; Sequence 24462, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24462
; LENGTH: 1676
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK099904
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-24462

Query Match 5.4%; Score 43.2; DB 6; Length 1676;
Best Local Similarity 52.8%; Pred. No. 0.6;
Matches 93; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 408 ATGAATAAAGTTTGTGCTGATCATTACCATGAGATATGAGATGCACTGCA 467
DB 285 AAGAGAGTTTGTGCTGATCATTACCATGAGATATGAGATGCACTGCA 226
QY 468 AATATCAAAAGAAATATAAATCAATATAGAGACAAACCATGTGATATTGTCCA 527
DB 225 ATAAAT 166
QY 528 TGTGCTCTTAAAGCAATGTATGTTATTTCTTGCAACCCCTACACAAAGCCACA 583
DB 165 GGAGATTAATACCGCAATGTGAAGTAGATCTAGAAAGGCACTAATTAGAGAGGA 110

RESULT 30

US-11-266-748A-395934/C
; Sequence 395934, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Johnston, Paul
; APPLICANT: Harkin, Paul
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 395934
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-395934

Query Match 5.2%; Score 42; DB 8; Length 1000;
Best Local Similarity 69.5%; Pred. No. 1;
Matches 57; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTACTACACCATTTTGTCTTCTCTGAAATTCATA 689
DB 738 CTAAGAGAGAGGCTGCCCGCATTAACCTCATTCTGTTCTCTCTCAAGTCCATA 679
QY 690 CTTCTTGTAGATAAGTTCTGT 711
DB 678 CTTCTTATATATCAATCTTT 657

RESULT 31

US-11-266-748A-466980
; Sequence 466980, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:

```

; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: FastSeq for Windows Version 3.3
; SEQ ID NO 466980
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-466980

Query Match          5.2%; Score 42; DB 8; Length 1000;
Best Local Similarity 69.5%; Pred. No. 1;
Matches 57; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 630 CTGAAGGAGAGGCTGTCCTTTTACTACACCATTTTAACTCTTTCTTCTGAATTCATTA 689
DB 263 CTAAAGGAGAGGCTGCCCCCGTATTAATCTCATTTCTGTTCTCTCCCAAGTCATTA 322
QY 690 CTTCTGTAGATTAAGTTCTGT 711
DB 323 CTTCTTATATATCATATTTCTTT 344

RESULT 32
US-11-283-329-219/C
; Sequence 219, Application US/11283329
; Publication No. US20060134670A1
; GENERAL INFORMATION:
; APPLICANT: Piu, Fabrice
; TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
; TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
; FILE REFERENCE: ACADIA.043A
; CURRENT APPLICATION NUMBER: US/11/283,329
; CURRENT FILING DATE: 2005-11-18
; PRIOR APPLICATION NUMBER: 60/629,811
; PRIOR FILING DATE: 2004-11-19
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 219
; LENGTH: 1417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)...(1172)
; OTHER INFORMATION: JNKL variant 2
US-11-283-329-219

Query Match          5.2%; Score 42; DB 8; Length 1417;
Best Local Similarity 69.5%; Pred. No. 1;
Matches 57; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
```

```

QY 630 CTGAAGGAGAGGCTGTCCTTTTACTACACCATTTTAACTCTTTCTTCTGAATTCATTA 689
DB 1155 CTAAAGGAGAGGCTGCCCCCGTATTAATCTCATTTCTGTTCTCTCCCAAGTCATTA 1096
QY 690 CTTCTGTAGATTAAGTTCTGT 711
DB 1095 CTTCTTATATATCATATTTCTTT 1074

RESULT 33
US-11-283-329-221/C
; Sequence 221, Application US/11283329
; Publication No. US20060134670A1
; GENERAL INFORMATION:
; APPLICANT: Piu, Fabrice
; TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
; TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
; FILE REFERENCE: ACADIA.043A
; CURRENT APPLICATION NUMBER: US/11/283,329
; CURRENT FILING DATE: 2005-11-18
; PRIOR APPLICATION NUMBER: 60/629,811
; PRIOR FILING DATE: 2004-11-19
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 221
; LENGTH: 1417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)...(1172)
; OTHER INFORMATION: JNKL variant 3
US-11-283-329-221

Query Match          5.2%; Score 42; DB 8; Length 1417;
Best Local Similarity 69.5%; Pred. No. 1;
Matches 57; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 630 CTGAAGGAGAGGCTGTCCTTTTACTACACCATTTTAACTCTTTCTTCTGAATTCATTA 689
DB 1155 CTAAAGGAGAGGCTGCCCCCGTATTAATCTCATTTCTGTTCTCTCCCAAGTCATTA 1096
QY 690 CTTCTGTAGATTAAGTTCTGT 711
DB 1095 CTTCTTATATATCATATTTCTTT 1074

RESULT 34
US-11-266-748A-349577/C
; Sequence 349577, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
```

```

; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 349577
; LENGTH: 1943
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-349577
```

```

Query Match          5.2%; Score 42; DB 8; Length 1943;
Best Local Similarity 69.5%; Pred. No. 1.2;
Matches 57; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
```

```

QY      630 CTGAAGGAGAGGCTGCTCTTTACTACACCAATTTTGTCTTCTTCTGATTCATTA 689
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      936 CTAAAGGAGAGGCTGCTCCCGGTATACCTCATTTCTTGTTCTCTCCCAAGTCATTA 877
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      690 CTTCCTGTAGATAGTTCGT 711
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      876 CTTCCTATATATCAATTCCTT 855
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 35

```

US-11-266-748A-382413/c
; Sequence 382413, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Johnston, Paul
; APPLICANT: Harkin, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 382413
; LENGTH: 1943
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-382413
```

```

Query Match          5.2%; Score 42; DB 8; Length 1943;
Best Local Similarity 69.5%; Pred. No. 1.2;
Matches 57; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
```

```

QY      630 CTGAAGGAGAGGCTGCTCTTTACTACACCAATTTTGTCTTCTTCTGATTCATTA 689
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      936 CTAAAGGAGAGGCTGCTCCCGGTATACCTCATTTCTTGTTCTCTCCCAAGTCATTA 877
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      690 CTTCCTGTAGATAGTTCGT 711
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      876 CTTCCTATATATCAATTCCTT 855
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 36

```

US-11-266-748A-432956
; Sequence 432956, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Johnston, Paul
; APPLICANT: Harkin, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 432956
; LENGTH: 1943
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-432956
```

```

Query Match          5.2%; Score 42; DB 8; Length 1943;
Best Local Similarity 69.5%; Pred. No. 1.2;
Matches 57; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY      630 CTGAAGGAGAGGCTGCTCTTTACTACACCAATTTTGTCTTCTTCTGATTCATTA 689
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      1008 CTAAAGGAGAGGCTGCTCCCGGTATACCTCATTTCTTGTTCTCTCCCAAGTCATTA 1067
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      690 CTTCCTGTAGATAGTTCGT 711
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      1068 CTTCCTATATATCAATTCCTT 1089
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 37

```

US-11-266-748A-24382/c
; Sequence 24382, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Johnston, Paul
; APPLICANT: Harkin, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
```

PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 24382
LENGTH: 3620
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-24382

Query Match 5.2%; Score 42; DB 8; Length 3620;
Best Local Similarity 69.5%; Pred. No. 1.5; Indels 0; Gaps 0;
Matches 57; Conservative 0; Mismatches 25;

QY 630 CTGAGAGAGAGGCTGCTCTTTACTACACCATTTTCTTTCTTGAATTCATTA 689
DB 2050 CTAAAGAGAGGCTGCTGCTGATTAATCTGTTCTCTCCATCCATCA 1991
QY 690 CTTCCTGTAGATAAGTTCGT 711
DB 1990 CTTCCTATATATCAATTCCTT 1969

RESULT 38
US-11-216-545-1069
Sequence 1069, Application US/11216545
Publication No. US20060135758A1
GENERAL INFORMATION:
APPLICANT: MONSANTO Technology, LLC
APPLICANT: McLaIRD, Paul L
APPLICANT: Tao, Nengbing
APPLICANT: Wu, Kunheng
TITLE OF INVENTION: Single Nucleotide Polymorphic Markers and Methods of Genotyping
FILE REFERENCE: 38-21 (53659)B
CURRENT APPLICATION NUMBER: US/11/216,545
CURRENT FILING DATE: 2005-08-31
PRIOR APPLICATION NUMBER: US 60/606,062
PRIOR FILING DATE: 2004-08-31
NUMBER OF SEQ ID NOS: 8783
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1069
LENGTH: 807
TYPE: DNA
ORGANISM: Glycine max
US-11-216-545-1069

Query Match 5.2%; Score 41.2; DB 8; Length 807;
Best Local Similarity 49.5%; Pred. No. 1.5; Indels 108; Gaps 0;
Matches 106; Conservative 0; Mismatches 108;

QY 296 ACATGACTGATGTCAAAAGGCAATATGCTCTGAATTTGATGAGCATTTCACC 355
DB 594 AATATGACTGATATATATATATATCCCTCCGTCCTGCTATTTATAGACATGTTTTT 653
QY 356 CTTTACCCCATGTATACATTTCTTCAGGATTCATCTATTAATTTATATGAAAA 415
DB 654 GTTATCTTATATTAAGATTTTATCTCTCTTGATATATTTATTTGCTAAAT 713
QY 416 GTTTTGTCTGATCATTCACATCAGATTAATCAGATTAATGACACATGATATCA 475
DB 714 ATCTTGATTTTCTCTTTCTCTCTATATAGATGAGAAATTTAAAAA 773
QY 476 AAGAAATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 509
DB 774 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 807

RESULT 39
US-11-266-748A-207992/c
Sequence 207992, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 207992
LENGTH: 570
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (462)..(462)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc.feature
LOCATION: (544)..(544)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc.feature
LOCATION: (564)..(564)
OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-207992

Query Match 5.1%; Score 41; DB 8; Length 570;
Best Local Similarity 49.3%; Pred. No. 1.5; Indels 110; Gaps 0;
Matches 107; Conservative 0; Mismatches 110;

QY 371 ACATTTCTCAGATTCATTAATTAATTTTGAAGTTTGTCTGAT 430
DB 345 ATATTTACAACGATATCTTCAAAATTTGAAAAATGATTCAGAACTTGGATCTATT 286
QY 431 CATTAACATCAGATTAATCAGATTAATGATCCACACTGATATCAAAAGAAATTAAC 490
DB 285 CATGTTTAATTAAGGCTTAAGTTGGGACTTTATCTTATATATCTATATAA 226
QY 491 AATCATTAAGACACACATGATTTTGTCCATCTGCTTTAAGCAATGTATG 550
DB 225 ATTTGTTATGCTTTAATTTTCTGATTTGTTTAAATGTTGTTTGTGTTTGTG 166
QY 551 TTAATTTGCAACCCCTACACAAAGGCCAAGAAAT 587
DB 165 TTTATTTGATCATCATCAATTAAGATGTTTAAATTT 129

RESULT 40
US-10-539-228-134/c

```
; Sequence 134, Application US/10539228
; Publication No. US20060154250A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: CHIR0052-101 (P023370.0003)
; CURRENT APPLICATION NUMBER: US/10/539,228
; PRIOR FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134
; LENGTH: 139326
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(139326)
; OTHER INFORMATION: n = A,T,C or G
US-10-539-228-134
```

```
Query Match
Best Local Similarity 5.1%; Score 40.8; DB 6; Length 139326;
Matches 90; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
```

```
QY 296 ACATGACCTGATGTCGCAAAAGGCGATTGCTCGAATTTGATGAGCACCATTACC 355
DB 58662 ACACCTTACAAATGGCAAAAGCTCGAATAGACATTTCTCCAAAGATATCTAATAATGCC 58603
QY 356 CTTTAGCCCATGTTTACATTTCTCGAGATTCATTAATTAATTTATGAAAA 415
DB 58602 AATGACCATATGAAAGATATTTACATCATTAATTAATTAATTAATTAATTAATTAAT 58543
QY 416 GTTTTGTCTGATCATTCATTCAGATCAGAAATATCAGAAATGCGACACTG 467
DB 58542 CATAAGAAAGCTGCTCATACCCATTAGATTAATTAATTAATTAATTAATTAATTAATTAAT 58491
```

```
RESULT 41
US-11-222-810-10
; Sequence 10, Application US/11222810
; Publication No. US20060089490A1
; GENERAL INFORMATION:
; APPLICANT: MUNNICH, Arnold
; APPLICANT: MELKI, Judith
; TITLE OF INVENTION: Spinal Muscular Atrophy Diagnostic Methods
; FILE REFERENCE: 2121-0140P
; CURRENT APPLICATION NUMBER: US/11/222,810
; PRIOR FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: US/09/109,082
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 08/545,196
; PRIOR FILING DATE: 1995-10-19
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 1582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-222-810-10
```

```
Query Match
Best Local Similarity 5.0%; Score 40.4; DB 8; Length 1582;
Matches 80; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
```

```
QY 364 CATGTTAATCTTCTCGAGATTCATTAATTAATTAATTAATTAATTAATTAATTAAT 423
DB 1423 CATGTTAATCTTCTTCTCGATTCATTAATTAATTAATTAATTAATTAATTAATTAAT 1482
QY 424 CTTGATCATTTACATCAGAAATATCAGAAATGATCCACTGAAATATCAAAAGAAATA 483
```

```
DB 1483 TTTTCTTAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1542
QY 484 AAACATAAATCATTTATTAAGACACAA 509
DB 1543 AAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1568
```

```
RESULT 42
US-11-222-810-12
; Sequence 12, Application US/11222810
; Publication No. US20060089490A1
; GENERAL INFORMATION:
; APPLICANT: MUNNICH, Arnold
; APPLICANT: MELKI, Judith
; TITLE OF INVENTION: Spinal Muscular Atrophy Diagnostic Methods
; FILE REFERENCE: 2121-0140P
; CURRENT APPLICATION NUMBER: US/11/222,810
; PRIOR FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: US/09/109,082
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 08/545,196
; PRIOR FILING DATE: 1995-10-19
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 1582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-222-810-12
```

```
Query Match
Best Local Similarity 5.0%; Score 40.4; DB 8; Length 1582;
Matches 80; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
```

```
QY 364 CATGTTAATCTTCTCGAGATTCATTAATTAATTAATTAATTAATTAATTAATTAAT 423
DB 1423 CATGTTAATCTTCTTCTCGATTCATTAATTAATTAATTAATTAATTAATTAATTAAT 1482
QY 424 CTTGATCATTTACATCAGAAATATCAGAAATGATCCACTGAAATATCAAAAGAAATA 483
DB 1483 TTTTCTTAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1542
QY 484 AAACATAAATCATTTATTAAGACACAA 509
DB 1543 AAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1568
```

```
RESULT 43
US-11-266-748A-41216/C
; Sequence 41216, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
```

```

; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 41216
; LENGTH: 557
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-41216

Query Match
Best Local Similarity 61.8%; Score 39.6; DB 8; Length 557;
Matches 63; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 696 TGTAGTAAAGTCTGTGTAAGAAACAGCTGTTATTATAGAAAACAATTATCCTTCATC 755
Db 233 TCGAGTAAATTTAATATATGATGATCTGTAGGAATATACATAAAATTTGTCAGTCATC 174
Qy 756 CACAGGAAATTCATTACTTAATGCCAAATTAATTACGTTTG 797
Db 173 CACAATTAAGTACATTAATTATGAGAAAAATTTACTATG 132

RESULT 44
US-11-266-748A-95203/c
; Sequence 95203, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95203
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-95203

Query Match
Best Local Similarity 5.0%; Score 39.6; DB 8; Length 559;
Matches 63; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 696 TGTAGTAAAGTCTGTGTAAGAAACAGCTGTTATTATAGAAAACAATTATCCTTCATC 755
Db 228 TCGAGTAAATTTAATATATGATGATCTGTAGGAATATACATAAAATTTGTCAGTCATC 169
Qy 756 CACAGGAAATTCATTACTTAATGCCAAATTAATTACGTTTG 797
Db 168 CACAATTAAGTACATTAATTATGAGAAAAATTTACTATG 127
```

```

RESULT 45
US-11-266-748A-148014
; Sequence 148014, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148014
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-148014

Query Match
Best Local Similarity 5.0%; Score 39.6; DB 8; Length 559;
Matches 63; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 696 TGTAGTAAAGTCTGTGTAAGAAACAGCTGTTATTATAGAAAACAATTATCCTTCATC 755
Db 332 TCGAGTAAATTTAATATATGATGATCTGTAGGAATATACATAAAATTTGTCAGTCATC 391
Qy 756 CACAGGAAATTCATTACTTAATGCCAAATTAATTACGTTTG 797
Db 392 CACAATTAAGTACATTAATTATGAGAAAAATTTACTATG 433

RESULT 46
US-11-266-748A-117427/c
; Sequence 117427, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
```

```

; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 117427
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-117427
```

```
Query Match          5.0%; Score 39.6; DB 8; Length 1000;
Best Local Similarity 61.8%; Pred. No. 3.9;
Matches 63; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
```

```
QY 696 TGTAGTAAGTCTCTGTAAGAAACAGCTGTGTTATTATAGAAAAACAATTATCTTCATC 755
DB 672 TGCAGGTAATTATTAATGATGCTGATCTGTAGAAATATACATAAAATTTGTCAGTCATC 613
QY 756 CACAGGAAATTCATTACTTAATGCCAAATATTAATGCTTTG 797
DB 612 CACAATTAACTACATTAATTATGAGAAAAATTTACTATG 571
```

```
RESULT 47
US-11-266-748A-159591
; Sequence 159591, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 159591
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-159591
```

```
Query Match          5.0%; Score 39.6; DB 8; Length 1000;
Best Local Similarity 61.8%; Pred. No. 3.9;
Matches 63; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
```

```
QY 696 TGTAGTAAGTCTCTGTAAGAAACAGCTGTGTTATTATAGAAAAACAATTATCTTCATC 755
DB 329 TGCAGGTAATTATTAATGATGCTGATCTGTAGAAATATACATAAAATTTGTCAGTCATC 388
```

```
QY 756 CACAGGAAATTCATTACTTAATGCCAAATATTAATGCTTTG 797
DB 389 CACAATTAACTACATTAATTATGAGAAAAATTTACTATG 430
```

```
RESULT 48
US-11-266-748A-222651/C
; Sequence 222651, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 222651
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-222651
```

```
Query Match          5.0%; Score 39.6; DB 8; Length 1000;
Best Local Similarity 61.8%; Pred. No. 3.9;
Matches 63; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
```

```
QY 696 TGTAGTAAGTCTCTGTAAGAAACAGCTGTGTTATTATAGAAAAACAATTATCTTCATC 755
DB 672 TGCAGGTAATTATTAATGATGCTGATCTGTAGAAATATACATAAAATTTGTCAGTCATC 613
QY 756 CACAGGAAATTCATTACTTAATGCCAAATATTAATGCTTTG 797
DB 612 CACAATTAACTACATTAATTATGAGAAAAATTTACTATG 571
```

```
RESULT 49
US-11-266-748A-289193/C
; Sequence 289193, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
```



```

; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 289193
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-289193
```

```
Query Match          5.0%; Score 39.6; DB 8; Length 1000;
Best Local Similarity 61.8%; Pred. No. 3.9;
Matches 63; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
```

```
Qy      696 TGTAGATAAGTCTCTGTAAGAAACAGCTGTGTATATAGAAAACAATTTATCCTTCATC 755
Db      672 TGCAGTAATTTAATTAATGACTGATCTGTAGGAATATACATTAATAATTTGTCAGTCATC 613

Qy      756 CACAGGAAATTCATTACTTAATGCCAAATTAATTCGTTTG 797
Db      612 CACAATTAAGTACATTAATTTATGAGAAAAATTTTACTATG 571
```

```

RESULT 50
US-11-266-748A-340622
; Sequence 340622, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkins, Paul
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 340622
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-340622
```

```
Query Match          5.0%; Score 39.6; DB 8; Length 1000;
Best Local Similarity 61.8%; Pred. No. 3.9;
Matches 63; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
```

```
Qy      696 TGTAGATAAGTCTCTGTAAGAAACAGCTGTGTATATAGAAAACAATTTATCCTTCATC 755
Db      329 TGCAGTAATTTAATTAATGACTGATCTGTAGGAATATACATTAATAATTTGTCAGTCATC 388

Qy      756 CACAGGAAATTCATTACTTAATGCCAAATTAATTCGTTTG 797
Db      389 CACAATTAAGTACATTAATTTATGAGAAAAATTTTACTATG 430
```

Search completed: July 19, 2006, 19:51:43
Job time : 169 secs